

```

RESULT 45
US-08-451-233-58
; Sequence 58, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPIISKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESS: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450

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RESULT 47
US-08-235-403-58
; Sequence 58, Application US/08235403
; Patent No. 6316003
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOOM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,403
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-403-58

Query Match 47.2%; Score 75; DB 3; Length 385;
Best Local Similarity 66.7%; Pred. No. 0.0038;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAPYIPM 24
DB 2 YGRKKRRQRRRLPSONQLMPSPM 25

RESULT 48

US-08-706-741B-87
Sequence 87, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-87

Query Match 37.7%; Score 60; DB 2; Length 32;
Best Local Similarity 48.1%; Pred. No. 0.038;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAPYIPMDD 27
DB 1 YGRKKRRQRRRGEIHHNIARHLAQIGD 27

RESULT 49

US-08-924-695A-87
Sequence 87, Application US/08924695A

Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-87

Query Match 37.7%; Score 60; DB 2; Length 32;
Best Local Similarity 48.1%; Pred. No. 0.038;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAPYIPMDD 27
DB 1 YGRKKRRQRRRGEIHHNIARHLAQIGD 27

RESULT 50

US-08-450-257-38
Sequence 38, Application US/08450257
Patent No. 5652122
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,257
FILING DATE: 25-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA: US 08/235,403
APPLICATION NUMBER: 28-APR-1994
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-257-38

Query Match 37.7%; Score 60; DB 1; Length 134;
Best Local Similarity 85.7%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 2 YGRKKRRQRRRPD 15

Search completed: February 9, 2005, 05:56:56
Job time : 32.0526 secs

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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:57:42 ; Search time 403.684 Seconds
(without alignments)
24.205 Million cell updates/sec

Title: US-10-032-361-7

Perfect score: 159

Sequence: 1 YRKKRRRRRLDLEMLAPYIPMDDFQL 30

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	101	63.5	20	14	US-10-287-670-25
3	101	63.5	34	16	US-10-901-583-9
4	101	63.5	54	9	US-09-922-958-5
5	101	63.5	409	15	US-10-425-833-8
6	101	63.5	466	15	US-10-425-833-9
7	101	63.5	538	15	US-10-425-833-6
8	101	63.5	542	15	US-10-264-049-2606
9	101	63.5	595	15	US-10-425-833-7
10	101	63.5	632	15	US-10-425-833-10
11	101	63.5	823	14	US-10-205-342-13
12	101	63.5	826	9	US-09-922-958-4
13	101	63.5	826	9	US-09-833-790-235

ALIGNMENTS

RESULT 1

US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09

Sequence 330, App
Sequence 330, App
Sequence 330, App
Sequence 4, Appli
Sequence 330, App
Sequence 23, Appl
Sequence 10, Appl
Sequence 9, Appli
Sequence 330, App
Sequence 14, Appl
Sequence 137, App
Sequence 9, Appli
Sequence 330, App
Sequence 2, Appli
Sequence 330, App
Sequence 18, Appl
Sequence 149, App
Sequence 5, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 71, Appl
Sequence 393, App
Sequence 611, App
Sequence 141, App
Sequence 142, App
Sequence 8, Appli
Sequence 399, App
Sequence 1, Appli
Sequence 37, Appl
Sequence 9, Appli
Sequence 13, Appl

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101 63.5 826 10 US-09-476-300-330
101 63.5 826 13 US-10-028-158-23
101 63.5 826 13 US-10-101-812-10
101 63.5 826 14 US-10-101-662A-9
101 63.5 826 14 US-10-017-754-330
101 63.5 826 14 US-10-115-987B-14
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101 63.5 826 14 US-10-423-419-2
101 63.5 826 15 US-10-283-017-330
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96 60.4 826 14 US-10-101-816-5
93 58.5 826 14 US-10-101-816-2
92 57.9 20 14 US-10-101-662A-15
92 57.9 20 14 US-10-287-670-15
89 56.0 19 14 US-10-313-643A-5
88 55.3 826 14 US-10-101-816-6
87 54.7 705 14 US-10-296-115-333
87 54.7 705 14 US-10-154-386-2
76.5 48.1 205 14 US-10-121-235-2
76.5 48.1 870 14 US-10-121-235-6
65 40.9 169 9 US-09-981-286A-7
64.5 40.6 195 9 US-09-949-780-6
61.5 38.7 870 14 US-10-101-816-4
60.5 38.1 23 13 US-10-024-935-10
60.5 38.1 23 13 US-10-024-935-11
60.5 38.1 23 15 US-10-603-409-10
60 37.7 22 9 US-10-603-409-11
60 37.7 22 9 US-09-949-196-8
52 60 37.7 22 14 US-10-311-111-34
52 60 37.7 22 14 US-10-083-815-71
54 59.5 37.4 1896 15 US-10-296-734-393
55 59.5 37.4 5747 15 US-10-296-734-405
56 59 37.1 685 15 US-10-369-493-611
57 58.5 36.8 17 10 US-09-847-946A-141
58 58.5 36.8 17 10 US-09-847-946A-142
59 58.5 36.8 20 13 US-10-024-935-8
60 58.5 36.8 20 15 US-10-603-409-8
61 58.5 36.8 1893 15 US-10-296-734-399
62 58 36.5 11 9 US-09-779-791A-1
63 58 36.5 11 9 US-09-780-070-37
64 58 36.5 11 9 US-09-815-108-9
65 58 36.5 11 9 US-09-886-404-13

;; PRIOR APPLICATION NUMBER: PCT/GB00/01826
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: GB9911047.0
;; PRIOR FILING DATE: 1999-05-12
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Motif
US-10-901-583-8

Query Match 63.5%; Score 101; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
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Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2

US-10-287-670-25
;; Sequence 25, Application US/10287670
;; Publication No. US20030150005A1
;; GENERAL INFORMATION:

;; APPLICANT: Kaelin Jr., et al.
;; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
;; TITLE OF INVENTION: Diagnostic and
;; FILE REFERENCE: 20363-009C1p
;; CURRENT APPLICATION NUMBER: US/10/287,670
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 10/101,662
;; PRIOR FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: 10/101,812
;; PRIOR FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: 10/101,816
;; PRIOR FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: 60/277,425
;; PRIOR FILING DATE: 2001-03-20
;; PRIOR APPLICATION NUMBER: 60/277,431
;; PRIOR FILING DATE: 2001-03-20
;; PRIOR APPLICATION NUMBER: 60/277,440
;; PRIOR FILING DATE: 2001-03-20
;; PRIOR APPLICATION NUMBER: 60/332,493
;; PRIOR FILING DATE: 2001-11-09
;; PRIOR APPLICATION NUMBER: 60/345,131
;; PRIOR FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 60/342,598
;; PRIOR FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 60/345,132
;; PRIOR FILING DATE: 2001-12-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 25
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-10-287-670-25

Query Match 63.5%; Score 101; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 3

US-10-901-583-9
;; Sequence 9, Application US/10901583
;; Publication No. US20050003452A1
;; GENERAL INFORMATION:
;; APPLICANT: Ratcliffe, Peter John
;; APPLICANT: Maxwell, Patrick Henry
;; APPLICANT: Pugh, Christopher William
;; TITLE OF INVENTION: Interaction Between the VHL Tumour
;; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
;; TITLE OF INVENTION: Relating thereto
;; FILE REFERENCE: 3547.1000-000
;; CURRENT APPLICATION NUMBER: US/10/901,583
;; CURRENT FILING DATE: 2004-07-29
;; PRIOR APPLICATION NUMBER: US/09/959,873
;; PRIOR FILING DATE: 2001-11-09
;; PRIOR APPLICATION NUMBER: PCT/GB00/01826
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: GB9911047.0
;; PRIOR FILING DATE: 1999-05-12
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

Query Match 63.5%; Score 101; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
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Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 4

US-09-922-958-5
;; Sequence 5, Application US/09922958
;; Patent No. US20020048794A1
;; GENERAL INFORMATION:
;; APPLICANT: POELLINGER, Lorenz
;; APPLICANT: PEREIRA, Teresa
;; APPLICANT: RUAS, Jorge
;; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR
;; FILE REFERENCE: 3743/49008
;; CURRENT APPLICATION NUMBER: US/09/922,958
;; CURRENT FILING DATE: 2001-08-07
;; PRIOR APPLICATION NUMBER: US 60/223,480
;; PRIOR FILING DATE: 2000-08-07
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 5
;; LENGTH: 54
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-922-958-5

Query Match 63.5%; Score 101; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 5

US-10-425-833-8

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; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HiP1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

Query Match          63.5%; Score 101; DB 15; Length 409;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 6
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HiP1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 466
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

Query Match          63.5%; Score 101; DB 15; Length 466;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 7
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HiP1-
; TITLE OF INVENTION: chimeric transactivator
```

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; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

Query Match          63.5%; Score 101; DB 15; Length 538;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 8
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2606
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-264-049-2606

Query Match          63.5%; Score 101; DB 15; Length 542;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 272 DLDLEMLAPYIPMDDDFQL 290

RESULT 9
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HiP1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 595
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;; TYPE: PRT
;; ORGANISM: ARTIFICIAL SEQUENCE
;; FEATURE:
;; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

Query Match 63.5%; Score 101; DB 15; Length 595;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 10
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF-1
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748USO
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 632
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

Query Match 63.5%; Score 101; DB 15; Length 632;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 11
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Protein: hypoxia-inducible factor-1 alpha
US-10-205-342-13

Query Match 63.5%; Score 101; DB 14; Length 823;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 12
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-4

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 13
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-235

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 14
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 15
US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-330

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

Db 556 DLDLEMLAPYIPMDDDFQL 574
RESULT 16
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-330

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 17
US-09-967-388-4
; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; TITLE OF INVENTION: WOUND HEALING
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 63.5%; Score 101; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 18
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476.300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-330

Query Match      63.5%; Score 101; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 19
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPICBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028.158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380.662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039.919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-158-23

Query Match      63.5%; Score 101; DB 13; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 20
US-10-101-812-10
; Sequence 10, Application US/10101812
; Publication No. US20020192737A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Pharmaceuticals and Methods for Treating Hypoxia and
; TITLE OF INVENTION: Screening Methods Thereof
; FILE REFERENCE: 20363-014
; CURRENT APPLICATION NUMBER: US/101.812
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431

```

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; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Target Peptide
US-10-101-812-10

Query Match      63.5%; Score 101; DB 13; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 21
US-10-101-662A-9
; Sequence 9, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/101.662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-662A-9

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Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 22

US-10-017-754-330

; Sequence 330, Application US/10017754
; Publication No. US20030054363A1

GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C18

; CURRENT APPLICATION NUMBER: US/10/017,754

; CURRENT FILING DATE: 2001-10-29

; NUMBER OF SEQ ID NOS: 2004

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 330

; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-017-754-330

Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 23

US-10-115-987B-14

; Sequence 14, Application US/10115987B

; Publication No. US20030148521A1

GENERAL INFORMATION:

; APPLICANT: Bell, John C.; Stojdl, David F.;
; APPLICANT: Gray, Douglas A.; Sonenberg,

; APPLICANT: Nahm, Lichty, Brian

; TITLE OF INVENTION: Conditionally Replicative and

; TITLE OF INVENTION: Conditionally Active Viruses

; FILE REFERENCE: 42630-0001

; CURRENT APPLICATION NUMBER: US/10/115,987B

; CURRENT FILING DATE: 2002-03-03

; PRIOR APPLICATION NUMBER: US60/281,781

; PRIOR FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: EditPad

; SEQ ID NO 14

; LENGTH: 826

; TYPE: PRT

; ORGANISM: homo Sapiens

; PUBLICATION INFORMATION:

; AUTHORS: Wang et al.

; JOURNAL: Proceedings of the National Academy of Sciences

; VOLUME: 92

; PAGES: 5510-5514

; DATE: 1995

US-10-115-987B-14

Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 24

US-10-287-670-9

; Sequence 9, Application US/10287670

; Publication No. US20030150005A1

GENERAL INFORMATION:

; APPLICANT: Kaelin Jr., et al.

; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and

; TITLE OF INVENTION: Diagnostic and

; TITLE OF INVENTION: Therapeutic Methods Thereof

; FILE REFERENCE: 20363-009CIP1

; CURRENT APPLICATION NUMBER: US/10/287,670

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 10/101,662

; PRIOR FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 10/101,812

; PRIOR FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 10/101,816

; PRIOR FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 60/277,425

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/277,431

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/277,440

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/332,493

; PRIOR FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: 60/345,131

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/342,598

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/345,132

; PRIOR FILING DATE: 2001-12-20

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-287-670-9

Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 25

US-10-113-872-330

; Sequence 330, Application US/10113872

; Publication No. US20030170255A1

GENERAL INFORMATION:

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113.872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-330

Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 26
US-10-423-419-2
; Sequence 2. Application US/10423419
; Publication No. US20030176349A1
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/10/423,419
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US/09/383,581
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-419-2

Query Match 63.5%; Score 101; DB 14; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 27
US-10-283-017-330
; Sequence 330. Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-017-330

Query Match 63.5%; Score 101; DB 15; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 28
US-10-901-583-18
; Sequence 18. Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-583-18

Query Match 63.5%; Score 101; DB 16; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 29
US-09-919-039-149
; Sequence 149. Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 401


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; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

Query Match      63.5%; Score 101; DB 10; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 30
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 137
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CD1
US-10-247-671-137

Query Match      63.5%; Score 101; DB 14; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 31
US-10-101-816-5
; Sequence 5, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493

Query Match      58.5%; Score 93; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00018;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

Query Match      60.4%; Score 96; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 6.9e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
   |||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 32
US-10-101-816-2
; Sequence 2, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-2
```

```
Qy 12 DLDLEMLAPYIPMDDDFOL 30
Db 556 DLDLEMLAAYIPMDDDFOL 574

RESULT 33
US-10-101-662A-15
; Sequence 15, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-287-670-15
Query Match 57.9%; Score 92; DB 14; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFOL 30
Db 1 DLDLEMLAXYIPMDDDFOL 19

RESULT 35
US-10-313-643A-5
; Sequence 5, Application US/10313643A
; Publication No. US20030153503A1
; GENERAL INFORMATION:
; APPLICANT: Klaus, Stephen J.
; APPLICANT: Lin, Al Y.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael P.
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekchov, Alexey G.
; TITLE OF INVENTION: METHODS OF INCREASING ENDOGENOUS ERYTHROPOIETIN (EPO)
; FILE REFERENCE: FPO601 US
; CURRENT APPLICATION NUMBER: US/10/313,643A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-313-643A-5
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Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Query Match	56.0%	Score 89;	DB 14;	Length 19;		
Best Local Similarity	89.5%	Pred. No. 1.2e-05;				
Matches	17;	Conservative	0;	Mismatches	2;	Indels
QY	12	DLDLEMLAPYIPMDDDFQL 30				
DB	1	DLDLEALAPYIPADDDFQL 19				
RESULT 36						
US-10-313-551A-5						
Sequence 5, Application US/10133551A						
Publication No. US20030176317A1						
GENERAL INFORMATION:						
APPLICANT: Guenzler-Pukall, Volkmar						
APPLICANT: Neff, Thomas B.						
APPLICANT: Wang, Qingjian						
APPLICANT: Arend, Michael						
APPLICANT: Flippin, Lee A.						
APPLICANT: Melekhov, Alexey G.						
TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA						
FILE REFERENCE: FP0600 US						
CURRENT APPLICATION NUMBER: US/10/313,551A						
CURRENT FILING DATE: 2002-12-06						
PRIOR APPLICATION NUMBER: US 60/337,082						
PRIOR FILING DATE: 2001-12-06						
PRIOR APPLICATION NUMBER: US 60/359,683						
PRIOR FILING DATE: 2002-02-25						
PRIOR APPLICATION NUMBER: US 60/349,659						
PRIOR FILING DATE: 2002-01-16						
PRIOR APPLICATION NUMBER: US 60/386,488						
PRIOR FILING DATE: 2002-06-05						
NUMBER OF SEQ ID NOS: 5						
SOFTWARE: PatentIn version 3.2						
SEQ ID NO 5						
LENGTH: 19						
TYPE: PRT						
ORGANISM: artificial sequence						
FEATURE:						
OTHER INFORMATION: synthetic peptide						
US-10-313-551A-5						
Query Match	56.0%	Score 89;	DB 14;	Length 19;		
Best Local Similarity	89.5%	Pred. No. 1.2e-05;				
Matches	17;	Conservative	0;	Mismatches	2;	Indels
QY	12	DLDLEMLAPYIPMDDDFQL 30				
DB	1	DLDLEALAPYIPADDDFQL 19				
RESULT 37						
US-10-101-816-6						
Sequence 6, Application US/10101816						
Publication No. US20030045686A1						
GENERAL INFORMATION:						
APPLICANT: Kaelin Jr., William G						
APPLICANT: Ivan, Mircea						
TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods						
FILE REFERENCE: 20363-008						
CURRENT APPLICATION NUMBER: US/10/101,816						
CURRENT FILING DATE: 2002-03-19						
PRIOR APPLICATION NUMBER: 60/277,425						
PRIOR FILING DATE: 2001-03-20						
PRIOR APPLICATION NUMBER: 60/277,431						
PRIOR FILING DATE: 2001-03-20						
PRIOR APPLICATION NUMBER: 60/277,440						
PRIOR FILING DATE: 2001-03-20						
PRIOR APPLICATION NUMBER: 60/332,493						
PRIOR FILING DATE: 2001-03-20						
PRIOR APPLICATION NUMBER: 60/332,493						
PRIOR FILING DATE: 2001-11-09						
PRIOR APPLICATION NUMBER: 60/345,200						
PRIOR FILING DATE: 2001-11-09						
PRIOR APPLICATION NUMBER: 60/345,131						
PRIOR FILING DATE: 2001-12-20						
PRIOR APPLICATION NUMBER: 60/342,598						
PRIOR FILING DATE: 2001-12-20						
PRIOR APPLICATION NUMBER: 60/345,132						
PRIOR FILING DATE: 2001-12-20						
PRIOR APPLICATION NUMBER: 60/332,334						
PRIOR FILING DATE: 2001-11-09						
NUMBER OF SEQ ID NOS: 16						
SOFTWARE: PatentIn Ver. 2.1						
SEQ ID NO 7						
LENGTH: 826						
TYPE: PRT						
ORGANISM: Artificial Sequence						
FEATURE:						
OTHER INFORMATION: Description of Artificial Sequence: H						

Query Match 56.0%; Score 89; DB 14; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYPMDDDFQL 30
DB 1 DLDLEALAPYPADDDFQL 19

RESULT 36
US-10-313-551A-5
Sequence 5, Application US/10133551A
Publication No. US20030176317A1
GENERAL INFORMATION:
APPLICANT: Guenzler-Pukall, Volkmar
APPLICANT: Neff, Thomas B.
APPLICANT: Wang, Qingjian
APPLICANT: Arend, Michael
APPLICANT: Flippin, Lee A.
APPLICANT: Melekhov, Alexey G.
TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
FILE REFERENCE: FP0600 US
CURRENT APPLICATION NUMBER: US/10/313,551A
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/337,082
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/359,683
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: US 60/349,659
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/386,488
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 19
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-313-551A-5

Query Match 56.0%; Score 89; DB 14; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYPMDDDFQL 30
DB 1 DLDLEALAPYPADDDFQL 19

RESULT 37
US-10-101-816-6
Sequence 6, Application US/10101816
Publication No. US20030045686A1
GENERAL INFORMATION:
APPLICANT: Kaelin Jr., William G
APPLICANT: Ivan, Mircea
TITLE OF INVENTION: Mutens of Hypoxia Inducible Factor Alpha and Methods
FILE REFERENCE: 20363-008
CURRENT APPLICATION NUMBER: US/10/101,816
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 60/277,425
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/277,431
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/277,440
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/332,493
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 826
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIF Mutain
US-10-101-816-6

Query Match 55.3%; Score 88; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.00092;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 39
US-10-296-115-933
; Sequence 933, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 933
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-933

Query Match 54.7%; Score 87; DB 15; Length 297;
Best Local Similarity 94.4%; Pred. No. 0.00043;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 LDLEMLAPYIPMDDDFQL 30
Db 166 LDLEMLAPYISMDDDFQL 183

RESULT 40
US-10-154-386-2
; Sequence 2, Application US/10154386
; Publication No. US20030026793A1
; GENERAL INFORMATION:
; APPLICANT: Angiogene Inc.
; TITLE OF INVENTION: HIPOXIA INDUCING FACTORS AND USES THEREOF FOR INDUCING ANGIOGENESIS
; FILE REFERENCE: 5600-81
; CURRENT APPLICATION NUMBER: US/10/154,386
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,630
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/354529
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-386-2

Query Match 54.7%; Score 87; DB 14; Length 705;
Best Local Similarity 94.4%; Pred. No. 0.0011;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 LDLEMLAPYIPMDDDFQL 30
Db 521 LDLEMLAPYISMDDDFQL 538

RESULT 41
US-10-121-235-2
; Sequence 2, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Maemura, Koji
; APPLICANT: GUY, Louis-Georges
; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
; FILE REFERENCE: 05433/037001
; CURRENT APPLICATION NUMBER: US/10/121,235
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/374,454
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 60/096,515
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-121-235-6

Query Match 48.1%; Score 76.5; DB 14; Length 870;
Best Local Similarity 80.0%; Pred. No. 0.041;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAPYIPMD-DDFQL 30
Db 523 ELDTLAPYIPMDGDFQL 542

RESULT 43
US-09-981-286A-7
; Sequence 7, Application US/09981286A
; Publication No. US20020192799A1
; GENERAL INFORMATION:
; APPLICANT: Watowich, Stanley J.
; APPLICANT: Weaver, Scott C.
; APPLICANT: Davey, Robert A.
; TITLE OF INVENTION: Drug Discovery Methods
; FILE REFERENCE: 265.00260101
; CURRENT APPLICATION NUMBER: US/09/981,286A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/240,187
; PRIOR FILING DATE: 2000-10-13

```
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of tat-CCD
US-09-981-286A-7

Query Match          40.9%; Score 65; DB 9; Length 169;
Best Local Similarity 81.2%; Pred. No. 0.3;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLE 16
   |||||
DB 2 YGRKKRRQRRRWKLE 17
   |||||

RESULT 44
US-09-949-780-6.
; Sequence 6, Application US/09949780
; Patent No. US20020061296A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020061296Aleborn, Mathieu H.M.
; APPLICANT: Voorhoeve, Pieter M.
; APPLICANT: Zhang, Ying-Hui
; APPLICANT: Leliveld, Sirik R.
; TITLE OF INVENTION: A Delivery Method for the Tumor Specific Apoptosis Inducing Activ
; TITLE OF INVENTION: Apoptin
; FILE REFERENCE: 2906-5001.IUS
; CURRENT APPLICATION NUMBER: US/09/949,780
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/236,117
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of XNvp3
US-09-949-780-6.

Query Match          40.6%; Score 64.5; DB 9; Length 195;
Best Local Similarity 66.7%; Pred. No. 0.41;
Matches 14; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 YGRKKRRQRRRLDLEMLAPY 21
   |||||
DB 38 YGRKKRRQRRRG-QISMAYPY 57
   |||||

RESULT 45
US-10-101-816-4
; Sequence 4, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
```

```
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-4

Query Match          38.7%; Score 61.5; DB 14; Length 870;
Best Local Similarity 70.0%; Pred. No. 5.4;
Matches 14; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQL 30
   :|||:
DB 523 ELDLETLAAYIPMDGEFQL 542
   :|||:

RESULT 46
US-10-024-935-10
; Sequence 10, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: YingNan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: 4-31664PI/prov
; CURRENT APPLICATION NUMBER: US/10/024,935
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-10

Query Match          38.1%; Score 60.5; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 0.16;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 YGRKKRRQRRRD-LDL 15
   |||||
DB 1 YGRKKRRQRRRLDL 16
   |||||

RESULT 47
US-10-024-935-11
; Sequence 11, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: YingNan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
```

; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: Interaction for Cancer Therapy
; CURRENT APPLICATION NUMBER: US/10/024,935
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-11

Query Match 38.1%; Score 60.5; DB 13; Length 23;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 14; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 YGRKKRRQRRR-DLDLEMLA 19
||||| : : ||
Db 1 YGRKKRRQRRRGETDHOYLA 20

RESULT 48
US-10-603-409-10
; Sequence 10, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: YingNan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: Interaction for Cancer Therapy
; CURRENT APPLICATION NUMBER: US/10/603,409
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/024,935
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/EP1 /15006
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-10

Query Match 38.1%; Score 60.5; DB 15; Length 23;
Best Local Similarity 87.5%; Pred. No. 0.16;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 YGRKKRRQRRR-DLDL 15
||||| : |||
Db 1 YGRKKRRQRRRGRDL 16

RESULT 49
US-10-603-409-11
; Sequence 11, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: YingNan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma

; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: Interaction for Cancer Therapy
; CURRENT APPLICATION NUMBER: US/10/603,409
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/024,935
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/EP1 /15006
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-11

Query Match 38.1%; Score 60.5; DB 15; Length 23;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 14; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 YGRKKRRQRRR-DLDLEMLA 19
||||| : : ||
Db 1 YGRKKRRQRRRGETDHOYLA 20

RESULT 50
US-09-949-196-8
; Sequence 8, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
; FILE REFERENCE: TO DNA DAMAGE
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-196-8

Query Match 37.7%; Score 60; DB 9; Length 22;
Best Local Similarity 85.7%; Pred. No. 0.18;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDL 14
||||| : |||
Db 1 YGRKKRRQRRRLFD 14

Search completed: February 9, 2005, 06:35:43
Job time : 404.684 secs

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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 166.842 Seconds
(without alignments)
69.544 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGKKRRRRRLDLEMLAPYIPMDDFQL 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003s:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	100.0	30	ABR82380	Abp57672 HIF-1 alp
2	144	90.6	1125	ABP57672	Abp57672 HIF-1 alp
3	144	90.6	1160	ABP57674	Abp57674 HIF-1 alp
4	142.5	89.6	1087	ABP57673	Abp57673 HIF-1 alp
5	142.5	89.6	1122	ABP57675	Abp57675 HIF-1 alp
6	124	78.0	28	AAO23532	AAO23532 Fluoresce
7	101	63.5	19	AAAB49912	AAAB49912 Human/mur
8	101	63.5	19	AAE30167	AAE30167 Peptide #
9	101	63.5	19	AAE30144	AAE30144 HIF1alpha
10	101	63.5	19	AAE30162	AAE30162 Peptide #
11	101	63.5	19	AAE30172	AAE30172 Human HIF
12	101	63.5	19	AAE30158	AAE30158 HIF-1alp
13	101	63.5	19	ABR82378	ABR82378 Hypoxia-1
14	101	63.5	19	ADP56728	ADP56728 Substrate
15	101	63.5	19	ADP79479	ADP79479 Hypoxia i
16	101	63.5	20	ABP55440	ABP55440 Hypoxia-i
17	101	63.5	20	ADP22337	ADP22337 HIF-1alp
18	101	63.5	29	AAO23481	AAO23481 Murine HI
19	101	63.5	29	AAO23499	AAO23499 Murine HI
20	101	63.5	34	AAE49913	AAE49913 Human/mur
21	101	63.5	34	AAE30161	AAE30161 Peptide #
22	101	63.5	34	AAE30151	AAE30151 HIF1alpha
23	101	63.5	54	AAE94637	AAE94637 HIF-1alp
24	101	63.5	54	AAO23490	AAO23490 Murine HI
25	101	63.5	54	AAO23530	AAO23530 Murine HI

26	101	63.5	54	7	AAO23528	Aao23528 Murine HI
27	101	63.5	54	7	AAO23529	Aao23529 Murine HI
28	101	63.5	116	3	AAAY94632	Aay94632 HIF-1alp
29	101	63.5	288	3	AAAY94633	Aay94633 HIF-1alp
30	101	63.5	301	3	AAAY94634	Aay94634 HIF-1alp
31	101	63.5	311	3	AAAY94631	Aay94631 HIF-1alp
32	101	63.5	409	8	ADO39389	Ado39389 Chimeric
33	101	63.5	444	4	AAAB68415	Aab68415 Amino aci
34	101	63.5	466	8	ADO39390	Ado39390 Chimeric
35	101	63.5	538	8	ADO39387	Ado39387 Chimeric
36	101	63.5	542	5	ABP41474	Abp41474 Human ova
37	101	63.5	595	8	ADO39388	Ado39388 Chimeric
38	101	63.5	613	3	AAAY94630	Aay94630 HIF-1alp
39	101	63.5	613	5	AAU77614	Aau77614 Human hyp
40	101	63.5	632	8	ADO39391	Ado39391 Chimeric
41	101	63.5	652	3	AAAY94629	Aay94629 HIF-1alp
42	101	63.5	669	3	AAAY84167	Aay84167 A variant
43	101	63.5	697	3	AAAY84166	Aay84166 A variant
44	101	63.5	701	3	AAAY84173	Aay84173 A variant
45	101	63.5	710	3	AAAY84172	Aay84172 A variant
46	101	63.5	724	3	AAAY84171	Aay84171 A variant
47	101	63.5	735	6	ABR82375	AbR82375 Hypoxia-i
48	101	63.5	735	8	ADN75066	Adn75066 Human hyp
49	101	63.5	749	3	AAAY84170	Aay84170 A variant
50	101	63.5	756	3	AAAY94635	Aay94635 HIF-1alp
51	101	63.5	789	3	AAAY84169	Aay84169 A variant
52	101	63.5	789	6	ADA18535	Ada18535 Human hyp
53	101	63.5	789	6	ADA18533	Ada18533 Human hyp
54	101	63.5	789	6	ADA18534	Ada18534 Human hyp
55	101	63.5	805	2	AAW06558	Aaw06558 Hypoxia i
56	101	63.5	810	5	ABBS7270	Abbs7270 Mouse iec
57	101	63.5	813	3	AAAY94636	Aay94636 HIF-1alp
58	101	63.5	823	6	ABR41951	AbR41951 Rat hypox
59	101	63.5	825	7	ADD44855	Add44855 Rat prote
60	101	63.5	826	2	AAW06557	Aaw06557 Human hyp
61	101	63.5	826	2	AAW06418	Aaw06418 Amino aci
62	101	63.5	826	2	AAAY06289	Aay06289 Human tra
63	101	63.5	826	3	AAAY69407	Aay69407 A wild ty
64	101	63.5	826	3	AAAY94640	Aay94640 Human hyp
65	101	63.5	826	4	AAAB76854	Aab76854 Human lun

ALIGNMENTS

RESULT 1	
ABR82380	
ID	ABR82380 standard; peptide; 30 AA.
XX	
AC	ABR82380;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.
KW	HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW	erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW	tranquillizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX	
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	Modified-site 20
FT	/label= HYP
FT	/note= "hydroxyproline"
XX	
XX	WO2003057820-A2.
XX	17-JUL-2003.
XX	
XX	04-OCT-2002; 2002WO-US031699.
PF	
XX	21-DEC-2001; 2001US-00032361.

```

XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX PI Mcgrath K;
XX DR WPI; 2003-645988/61.
XX XX Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX PS Claim 2; Page 9; 37pp; English.
XX CC The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
CC containing the oxygen-dependent degradation sequence of HIF-1 alpha
XX SQ Sequence 30 AA;
XX Query Match 100.0%; Score 159; DB 6; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-15;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRKKRRQRRRLDLEMLAPYIPMDDDFQL 30
DB 1 YGRKKRRQRRRLDLEMLAPYIPMDDDFQL 30
XX RESULT 2
XX ABP57672
XX ID ABP57672 standard; protein; 1125 AA.
XX AC ABP57672;
XX DT 30-APR-2003 (first entry)
XX DE HIF-1 alpha related fusion protein pCH/TAT/3-0 SEQ ID NO:39.
XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
XX hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
XX tumour; nuclear localisation signal; oxygen dependent degradation domain;
XX NLS; ODD; fusion protein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200299104-A1.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-00169948.
XX PR 05-JUN-2001; 2001JP-00169949.
XX XX (POKX ) POLA CHEM IND INC.
XX PA (HIRA/) HIRAOKA M.
XX PA (KOND/) KONDOH S.
XX XX Hiraoka M, Kondoh S, Harada H;
XX PI WPI; 2003-148670/14.
XX DR N-PSDB; ABZ76624.
XX XX New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX Example 3; Page 75-78; 144pp; Japanese.
XX The present invention describes DNA encoding a hypoxia-inducible factor 1
XX alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
XX see ABP57669) (I), or encoding a fusion protein containing at least 16
XX residues of (I), a nuclear localisation signal (NLS), and another
XX protein, and imparting relative stability under specific conditions of
XX oxygen concentration within the cell. Also described: (1) vectors
XX containing the DNA; (2) cells transformed by the vectors; (3) producing
XX the fusion protein by culture of the transformed cells; (4) detecting
XX hypoxic conditions in cells by monitoring the stability of the protein
XX fused to (I) in cells transformed by vectors containing the DNA; (5)
XX regulating the stability of proteins within the cell by transformation
XX with the DNA; (6) inhibiting the development of cells under hypoxic
XX conditions, using the fusion protein; (7) fusion proteins encoded by the
XX DNA; and (8) stabilisation of cells under specific conditions of oxygen
XX tension. (I) has cytostatic activity, and can be used for the
XX stabilisation of a cytotoxic protein within cells in hypoxic regions of a
XX solid tumour, and in gene therapy. (I) can be used in industrial
XX microbial fermentation, and in medicine, especially in the treatment of
XX tumours containing hypoxic regions. The present sequence represents a
XX fusion protein from the present invention
XX SQ Sequence 1125 AA;
XX Query Match 90.6%; Score 144; DB 6; Length 1125;
XX Best Local Similarity 75.0%; Pred. No. 1.8e-11;
XX Matches 30; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 1 YGRKKRRQRRR-----DLDLEMLAPYIPMDDDFQL 30
DB 11 YGRKKRRQRRRRNPFSTQTDLDLEMLAPYIPMDDDFQL 50
XX RESULT 3
XX ABP57674
XX ID ABP57674 standard; protein; 1160 AA.
XX AC ABP57674;
XX DT 30-APR-2003 (first entry)
XX DE HIF-1 alpha related fusion protein pBAD/3-0 SEQ ID NO:43.
XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
XX hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
XX tumour; nuclear localisation signal; oxygen dependent degradation domain;
XX NLS; ODD; fusion protein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200299104-A1.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-00169948.
XX PR 05-JUN-2001; 2001JP-00169949.
XX XX (POKK ) POLA CHEM IND INC.
XX PA (HIRA/) HIRAOKA M.
XX PA (KOND/) KONDOH S.
XX XX Hiraoka M, Kondoh S, Harada H;
XX PI WPI; 2003-148670/14.
XX DR N-PSDB; ABZ76626.
XX XX New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT

```



```

PT and improvement of microbial fermentation.
XX
PS Example 3; Page 95-99; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (1), or encoding a fusion protein containing at least 16
CC residues of (1), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (1) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (1) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (1) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1160 AA;
Query Match 90.6%; Score 144; DB 6; Length 1160;
Best Local Similarity 75.0%; Pred. No. 1.9e-11; Mismatches 0; Indels 10; Gaps 1;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 YGKRRRRR-----DLLEMLAPYIPMDDDFQL 30
| | | | | | | | | | | | | | | | | |
DB 46 YGKRRRRRRSNPFSTQTDLDLEMLAPYIPMDDDFQL 85
| | | | | | | | | | | | | | | | | |

RESULT 4
ABP57673
ID ABP57673 standard; protein; 1087 AA.
XX
AC ABP57673;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/557-574 SEQ ID NO:41.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK ) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76625.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic

```

```

PT conditions to proteins within the cell, useful for treatment of cancer
XX and improvement of microbial fermentation.
XX
PS Example 3; Page 85-88; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (1), or encoding a fusion protein containing at least 16
CC residues of (1), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (1) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (1) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (1) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1087 AA;
Query Match 89.6%; Score 142.5; DB 6; Length 1087;
Best Local Similarity 93.5%; Pred. No. 2.9e-11;
Matches 29; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 YGKRRRRR-----RRRDLDLEMLAPYIPMDDDFQL 30
| | | | | | | | | | | | | | | | | |
DB 11 YGKRRRRRRRRSLDLEMLAPYIPMDDDFQL 41
| | | | | | | | | | | | | | | | | |

RESULT 5
ABP57675
ID ABP57675 standard; protein; 1122 AA.
XX
AC ABP57675;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/557-574 SEQ ID NO:45.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK ) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76627.
XX

```


XX Claim 13; Page 49; 56pp; English.

XX The present invention describes a novel assay for use in identifying

CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible

CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises

CC contacting the VHL protein, the HIF-1alpha subunit and the putative

CC modulator under conditions where the former two would normally complex.

CC Modulators of this type are useful in the treatment of cancer and

CC ischaemic conditions such as coronary, cerebral and vascular

CC insufficiency

XX Sequence 19 AA;

XX Query Match 63.5%; Score 101; DB 4; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 3e-07;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 8

AAE30167

ID AAE30167 standard; peptide; 19 AA.

XX AAE30167;

XX 24-FEB-2003 (first entry)

XX Peptide #7 used to block HIF-1alpha/pVHL interaction.

XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

XX wound healing; ischaemia; transplantation; blood pressure; gene therapy.

XX Unidentified.

XX WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

XX 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

XX WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

XX auto-, allo-, and xeno-transplantation, systemic high blood pressure,

XX cancer, or inflammatory disorders.

XX Example 1; Page 247; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

CC used to design double stranded RNAs for use in RNA interference. They are

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL

CC interaction. This sequence is used in the invention

XX Sequence 19 AA;

XX Query Match 63.5%; Score 101; DB 6; Length 19;

XX Sequence 19 AA;

XX Query Match 63.5%; Score 101; DB 6; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 3e-07;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 9

AAE30144

ID AAE30144 standard; peptide; 19 AA.

XX AAE30144;

XX 24-FEB-2003 (first entry)

XX HIF1alpha subunit antagonist #1.

XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

XX wound healing; ischaemia; transplantation; blood pressure; gene therapy;

XX antagonist.

XX Unidentified.

XX Key Location/Qualifiers

XX Modified-site 2 /label= Hyp

XX WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

XX 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

XX WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

XX auto-, allo-, and xeno-transplantation, systemic high blood pressure,

XX cancer, or inflammatory disorders.

XX Claim 49; Page 196; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

CC used to design double stranded RNAs for use in RNA interference. They are

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is HIF1alpha subunit antagonist. This

CC sequence is used in the invention

XX Sequence 19 AA;

XX Query Match 63.5%; Score 101; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 10
AAE30162
ID AAE30162 standard; peptide; 19 AA.
XX
AC AAE30162;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #2 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
XX wound healing; ischaemia; transplantation; blood pressure; gene therapy.
OS Unidentified.
XX WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
XX
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX WPI; 2003-018808/01.
XX
XX Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 246; 256pp; English.
XX
XX The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 11
AAE30172
ID AAE30172 standard; peptide; 19 AA.
XX
AC AAE30172;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human HIF1-alpha peptide #2.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
XX wound healing; ischaemia; transplantation; blood pressure; gene therapy;
XX human; HIF1-alpha.
OS Homo sapiens.
XX WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
XX
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX WPI; 2003-018808/01.
XX
XX Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Disclosure; Page 252; 256pp; English.
XX
XX The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is human HIF1-alpha peptide. This sequence
CC is used in the invention
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 12
AAE30158
ID AAE30158 standard; peptide; 19 AA.
XX
AC AAE30158;
XX
DT 24-FEB-2003 (first entry)
XX
DE HIF-1alpha pVHL minimal binding domain.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO200274981-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 21-MAR-2002; 2002WO-GB001381.
 XX
 PR 21-MAR-2001; 2001GB-00007123.
 PR 02-AUG-2001; 2001GB-00018952.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
 PI WPI; 2003-018808/01.
 XX
 PT Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.
 XX
 PS Example 1; Page 245; 256pp; English.
 XX
 CC The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
 CC This sequence is used in the invention
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 63.5%; Score 101; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 13
 ABR82378
 ID ABR82378 standard; peptide; 19 AA.
 AC ABR82378;
 XX
 XX 06-NOV-2003 (first entry)
 DT
 DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
 XX
 KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
 KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
 KW tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 9
 FT /label= Hyp
 FT /note= "hydroxyproline"

XX WO2003057820-A2.
 PN 17-JUL-2003.
 XX
 PD 04-OCT-2002; 2002WO-US031699.
 PF
 XX 21-DEC-2001; 2001US-00032361.
 PR
 XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA
 XX Mcgrath K;
 PI WPI; 2003-645988/61.
 XX
 DR Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 XX ubiquitination, and activator of vascular endothelial growth factor
 PT transcription useful for treating tissue injuries including wounds,
 PT surgical incisions.
 XX
 PS Claim 2; Page 8; 37pp; English.
 XX
 CC The invention relates to peptide inhibitors of hypoxia-inducible factor
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor
 CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
 CC for treating tissue injuries including wounds, surgical incisions,
 CC chronic wounds, heart disease and stroke. The present sequence represents
 CC a specific example of HIF-1 alpha peptide inhibitor, containing the
 CC oxygen-dependent degradation sequence of HIF-1 alpha
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 63.5%; Score 101; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 14
 ADP56728
 ID ADP56728 standard; peptide; 19 AA.
 XX
 AC ADP56728;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
 XX
 KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
 KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
 KW human; HIF-PH.
 XX
 OS Homo sapiens.
 XX
 PN WO2004052285-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 05-DEC-2003; 2003WO-US038690.
 XX
 PR 06-DEC-2002; 2002US-0431351P.
 PR 06-JUN-2003; 2003US-0476331P.
 PR 06-JUN-2003; 2003US-0476726P.
 PR 04-DEC-2003; 2003US-00729167.
 XX
 XX (FIBR-) FIBROGEN INC.
 PA
 XX Fournay PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
 PI Seeley TW;

XX WPI; 2004-468689/44.
 XX Regulating fat metabolism or fat metabolic process in subjects, by
 PT stabilizing human forebrain fibroblasts alpha in subject, thus regulating
 PT fat metabolism or fat metabolic process in subject.
 XX
 PS Example 9; SEQ ID NO 1; 66pp; English.
 XX
 CC The invention relates to a novel method for regulating fat metabolism or
 CC the fat metabolic process in a subject which comprises stabilising human
 CC forebrain fibroblast HIF1alpha (hypoxia inducible factor alpha subunit) in
 CC the subject, or administering a compound that inhibits HIF hydroxylase
 CC activity, thus regulating fat metabolism or the fat metabolic process in
 CC the subject. The method of the invention may be useful for regulating fat
 CC metabolism or a fat metabolic process in a subject. The subject is an
 CC animal, preferably a mammal, more preferably human and the method is
 CC performed in a human cell, tissue or organ. The method may be useful for
 CC treating or preventing atherosclerosis, diabetes and obesity in a
 CC subject. The current sequence is that of the substrate peptide of the
 CC invention which is used during a screening assay of human HIF prolyl
 CC hydroxylase (HIF-PH).
 XX
 SQ Sequence 19 AA;
 Query Match 63.5%; Score 101; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 15
 ADP79479
 ID ADP79479 standard; peptide; 19 AA.
 XX
 AC ADP79479;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Hypoxia inducible factor prolyl hydroxylase substrate peptide.
 XX
 KW Human; Hypoxia inducible factor prolyl hydroxylase; Glucose metabolism;
 KW antidiabetic; anorectic; hypotensive; antilipemic; nephrotropic;
 KW neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2004052284-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 05-DEC-2003; 2003WO-US038689.
 XX
 PR 06-DEC-2002; 2002US-0431351P.
 XX
 PR 06-JUN-2003; 2003US-0476331P.
 XX
 PR 06-JUN-2003; 2003US-0476726P.
 XX
 PR 04-DEC-2003; 2003US-00729704.
 XX
 XX (FIBER-) FIBROGEN INC.
 XX
 XX Guenzler-Pukall V, Klaus SJ, Langeetmo Farobok I, Seeley TW;
 XX WPI; 2004-468688/44.
 XX
 XX Regulating glucose metabolism or glucose metabolic process in subject,
 PT involves stabilizing hypoxia inducible factor alpha in subject, or
 PT administering to subject compound inhibiting hypoxia inducible factor
 PT hydroxylase activity.
 XX

PS Example 14; SEQ ID NO 5; 74pp; English.
 XX
 CC The present sequence is that of a substrate peptide for hypoxia inducible
 CC factor (HIF) prolyl hydroxylase. It was used in an example from the
 CC invention for the identification of compounds useful for HIF alpha
 CC stabilisation. The invention provides methods and compounds for
 CC regulating glucose metabolism by stabilising HIF alpha, especially by
 CC administering a compound that inhibits HIF hydroxylase activity. The
 CC method of stabilising HIF alpha is used in claimed methods for achieving
 CC glucose homeostasis, decreasing blood glucose levels, decreasing glycated
 CC haemoglobin levels, altering expression of a glucose regulatory factor,
 CC altering expression of a glycolytic factor, treating or preventing
 CC diabetes, treating or preventing a disorder associated with increased
 CC blood glucose levels (especially diabetes, hyperglycaemia, obesity,
 CC hypertension, hyperlipidaemia, neuropathy, retinopathy, retinopathy,
 CC impaired glucose tolerance, atherosclerosis and vascular disease),
 CC treating or preventing a condition associated with diabetes, decreasing
 CC blood triglyceride levels, reducing insulin resistance, and increasing
 CC glycaemic control in a subject.
 XX
 SQ Sequence 19 AA;
 Query Match 63.5%; Score 101; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e-07; 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 16
 ABP55440
 ID ABP55440 standard; peptide; 20 AA.
 XX
 AC ABP55440;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Hypoxia-inducible factor (HIF) 1 alpha peptide.
 XX
 KW Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
 KW ischaemic-related disorder; hypoxia-inducible factor-related disorder;
 KW prolyl hydroxylation; HIF; hypoxic; ischaemic; vasotropic; cardiac;
 KW neuroprotective; cytotactic; thrombolytic; antidiabetic; nephrotropic;
 KW myocardial infarction; heart disease; stroke; cancer; diabetes;
 KW cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
 KW renal failure; angiogenesis; vascularisation; prolyl hydroxylase.
 XX
 OS Homo sapiens.
 XX
 PN WO200274249-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002WO-US008886.
 XX
 PR 20-MAR-2001; 2001US-0277425P.
 XX
 PR 20-MAR-2001; 2001US-0277431P.
 XX
 PR 20-MAR-2001; 2001US-0277440P.
 XX
 PR 09-NOV-2001; 2001US-0332334P.
 XX
 PR 09-NOV-2001; 2001US-0332493P.
 XX
 PR 09-NOV-2001; 2001US-0345200P.
 XX
 PR 20-DEC-2001; 2001US-0342598P.
 XX
 PR 20-DEC-2001; 2001US-0345131P.
 XX
 PR 20-DEC-2001; 2001US-0345132P.
 XX
 PR 19-MAR-2002; 2002US-00101812.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.

XX PI Kaelin WG, Ivan M;
 XX WPI; 2003-058330/05.
 XX
 XX Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
 PT myocardial infarction, stroke, cancer, thrombosis or renal failure, by
 PT administering a modulator prolyl hydroxylation of hypoxia-inducible
 PT factor (HIF).
 XX
 XX Disclosure; Page 26; 128pp; English.
 XX
 XX The present invention describes a method for treating or preventing a
 CC hypoxic-related disorder, ischemic-related disorder, or hypoxia-
 CC inducible factor (HIF)-related disorder in a subject by administering to
 CC the subject a compound that modulates prolyl hydroxylation of HIF, such
 CC that the hypoxic-, ischemic-, or HIF-related disorder is treated,
 CC prevented, reversed or stabilised. HIF related sequences can have
 CC vasotropic, cardiant, cerebroprotective, cytostatic, thrombolytic,
 CC antidiabetic, and nephrotropic activities. The method is useful for
 CC treating hypoxia-related disorder, ischemic-related disorder or HIF-
 CC related disorder. In particular, the hypoxic- or ischemic-related
 CC disorder is an acute event (e.g. myocardial infarction, heart disease,
 CC stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
 CC event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
 CC especially a chronic event not caused by tissue scarring. The method is
 CC also useful for increasing angiogenesis or vascularisation. The present
 CC sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
 CC peptide which is given in the exemplification of the present invention
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 63.5%; Score 101; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 17
 ADO22337
 ID ADO22337 standard; peptide; 20 AA.
 AC ADO22337;
 DT 12-AUG-2004 (first entry)
 XX
 DE HIF-1alpha ligand binding site peptide SEQ ID NO:15.
 XX
 KW transgenic; transgenic non-human animal; light-generating fusion protein;
 KW ligand binding site; light-generating polypeptide moiety;
 KW hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
 KW respiratory; cytostatic; vasotropic; virucide; hypoxic condition; cancer;
 KW ischaemia; viral infection; drug screening; drug discovery;
 KW ligand binding site peptide.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004042361-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US035154.
 XX
 PR 04-NOV-2002; 2002US-00287670.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Kaelin WG, Livingston DM, Kim T;
 XX

DR WPI; 2004-400725/37.
 XX
 XX New transgenic non-human animal comprising light-generating fusion
 PT protein, useful in diagnosing and treating hypoxic conditions, cancer,
 PT ischemia and viral infections and in drug screening and discovery.
 XX
 XX Disclosure; SEQ ID NO 15; 111pp; English.
 XX
 CC The present invention describes a transgenic non-human animal comprising
 CC a recombinant nucleic acid molecule stably integrated into the genome of
 CC the animal, where the molecule encodes a light-generating fusion protein
 CC comprising a ligand binding site and a light-generating polypeptide
 CC moiety. Also described: (1) an isolated cell of the animal; (2) producing
 CC a transgenic non-human animal; (3) identifying a compound capable of
 CC modifying an activity of hypoxia-inducible factor (HIF) 1 alpha; and (4)
 CC detecting hypoxic tissue. The compound has respiratory, cytostatic,
 CC vasotropic and virucide activities. The transgenic non-human animal,
 CC light-generating fusion protein, agents, kits and compositions are useful
 CC in diagnosing and treating hypoxic conditions, cancer, ischaemia and
 CC viral infections and in drug screening and discovery. The present
 CC sequence represents a HIF-1alpha ligand binding site peptide, which is
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 63.5%; Score 101; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 18
 AAO23481
 ID AAO23481 standard; peptide; 29 AA.
 XX
 AC AAO23481;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Murine HIF-1alpha protein mutant fragment.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW mutant.
 XX
 OS Mus sp.
 OS
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333p.
 PR 27-NOV-2002; 2002US-0429307p.
 XX
 PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstrom M;
 XX
 XX WPI; 2003-712876/67.
 XX
 XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 PS Claim 39; Page 93; 96pp; English.
 XX

CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a specific example
 CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
 CC related conditions

XX Sequence 29 AA;

Query Match 63.5%; Score 101; DB 7; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 19

AAO23499 AAO23499 standard; peptide; 29 AA.

XX AAO23499;

DT 12-FEB-2004 (first entry)

XX Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).

KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD.

XX Mus sp.

XX WO2003074560-A2.

XX 12-SEP-2003.

XX 05-MAR-2003; 2003WO-SE000372.

XX 05-MAR-2002; 2002US-0361333P.

XX 27-NOV-2002; 2002US-0429307P.

XX (ANGI-) ANGIOGENETICS SWEDEN AB.

XX Pereira T, Poellinger L, Hellstroem M;
 PI WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 CC angiogenesis, or treating a condition associated with HIF-1alpha
 CC underexpression in a cell, a group of cells, or an organism, e.g.
 CC ischemia or inflammation.

XX Example 6; Fig 19; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or

CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein

XX Sequence 29 AA;

Query Match 63.5%; Score 101; DB 7; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 20

AAO49913 AAB49913 standard; peptide; 34 AA.

ID AAB49913

AC AAB49913;

XX 06-MAR-2001 (first entry)

XX Human/murine HIF-1alpha subunit conserved motif #9.

XX Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;

XX hypoxia inducible factor-1; cancer; ischaemia.

XX Mus sp.

XX Homo sapiens.

XX WO200069908-A1.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-GB001826.

XX 12-MAY-1999; 99GB-00011047.

XX (ISIS-) ISIS INNOVATION LTD.

XX Ratcliffe PJ, Maxwell PH, Pugh CW;

XX WPI; 2001-025006/03.

XX Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
 CC subunit interaction modulators for treating ischemia by contacting a VHL
 CC protein and an HIF subunit protein with a putative modulator.

XX Claim 14; Page 50; 56pp; English.

XX The present invention describes a novel assay for use in identifying
 CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
 CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
 CC contacting the VHL protein, the HIF-1alpha subunit and the putative
 CC modulator under conditions where the former two would normally complex.
 CC Modulators of this type are useful in the treatment of cancer and
 CC ischaemic conditions such as coronary, cerebral and vascular
 CC insufficiency

XX Sequence 34 AA;

Query Match 63.5%; Score 101; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 DB 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 21

AAE30161
 ID AAE30161 standard; peptide; 34 AA.

XX AAE30161;

DT 24-FEB-2003 (first entry)

XX Peptide #1 used to block HIF-1alpha/pVHL interaction.

XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.

XX Unidentified.

XX WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

PI WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.

XX Example 1; Page 246; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
 CC interaction. This sequence is used in the invention

XX Sequence 34 AA;

Query Match 63.5%; Score 101; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 DB 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 22

AAE30151
 ID AAE30151 standard; peptide; 34 AA.

XX

AC

AAE30151;

XX 24-FEB-2003 (first entry)

XX HIF1alpha subunit antagonist #8.

XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
 KW antagonist.

XX Unidentified.

XX WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

PI WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.

XX Disclosure; Page 239; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is HIF1alpha subunit antagonist. This
 CC sequence is used in the invention

XX Sequence 34 AA;

Query Match 63.5%; Score 101; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 DB 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 23

AAAY94637

ID AAY94637 standard; protein; 54 AA.

XX AAY94637;

XX 15-AUG-2000 (first entry)

XX HIF-1alpha variant protein sequence HIF-1alpha/531-584.

XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX

us-10-032-361-7.rag

05-MAR-2003; 2003WO-SE000372.
05-MAR-2002; 2002US-0361333P.
27-NOV-2002; 2002US-0429307P.
(ANGI-) ANGIOGENETICS SWEDEN AB.
Pereira T, Poellinger L, Hellstroem M;
WPI; 2003-712876/67.
New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing angiogenesis, or treating a condition associated with HIF-1alpha underexpression in a cell, a group of cells, or an organism, e.g. ischemia or inflammation.
Example 4; Fig 4; 96pp; English.
The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein that has (a) an altered transactivation capacity and improved stability at normoxia. The HIF-1alpha protein, polynucleotide, vector, and pharmaceutical composition are useful for increasing angiogenesis, or interfering with a normal response to reoxygenation following hypoxia, or treating a condition associated with HIF-1alpha underexpression in a cell, a group of cells, or an organism, e.g. ischaemia, diabetic retinopathy, inflammation, coronary heart disease, rheumatoid arthritis, stroke. The proteins and pharmaceutical compositions are also useful for mimicking the hypoxic response or artificially inducing a hypoxic response in a cell, group of cells, or organism, inducing vascular formation or vascular development in a cell or a group of cells, increasing angiogenetic activity in a cell, or influencing erythropoietin production, metabolism, or an inflammatory response in a cell, a group of cells, or an organism. The present sequence represents a N-TAD region of a murine HIF-1 alpha protein
Sequence 54 AA;
Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 DLDLEMLAPYIPMDDDFQL 30
Db 25 DLDLEMLAPYIPMDDDFQL 43
RESULT 25
AAO23530
ID AAO23530 standard; peptide; 54 AA.
XX AC AAO23530;
XX DT 12-FEB-2004 (first entry)
XX DE Murine HIF-1alpha protein N-TAD region mutant fragment Q572A.
XX KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
XX KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
XX KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
XX KW N-TAD; mutant.
XX OS Mus sp.
XX PN WO2003074560-A2.
XX PD 12-SEP-2003.
XX PF 05-MAR-2003; 2003WO-SE000372.
XX PN 05-MAR-2002; 2002US-0361333P.
XX PR 27-NOV-2002; 2002US-0429307P.

us-10-032-361-7.rag

05-MAR-2003; 2003WO-SE000372.
05-MAR-2002; 2002US-0361333P.
27-NOV-2002; 2002US-0429307P.
(ANGI-) ANGIOGENETICS SWEDEN AB.
Pereira T, Poellinger L, Hellstroem M;
WPI; 2003-712876/67.
New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing angiogenesis, or treating a condition associated with HIF-1alpha underexpression in a cell, a group of cells, or an organism, e.g. ischemia or inflammation.
Example 4; Fig 4; 96pp; English.
The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein that has (a) an altered transactivation capacity and improved stability at normoxia. The HIF-1alpha protein, polynucleotide, vector, and pharmaceutical composition are useful for increasing angiogenesis, or interfering with a normal response to reoxygenation following hypoxia, or treating a condition associated with HIF-1alpha underexpression in a cell, a group of cells, or an organism, e.g. ischaemia, diabetic retinopathy, inflammation, coronary heart disease, rheumatoid arthritis, stroke. The proteins and pharmaceutical compositions are also useful for mimicking the hypoxic response or artificially inducing a hypoxic response in a cell, group of cells, or organism, inducing vascular formation or vascular development in a cell or a group of cells, increasing angiogenetic activity in a cell, or influencing erythropoietin production, metabolism, or an inflammatory response in a cell, a group of cells, or an organism. The present sequence represents a N-TAD region of a murine HIF-1 alpha protein
Sequence 54 AA;
Query Match 63.5%; Score 101; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 DLDLEMLAPYIPMDDDFQL 30
Db 26 DLDLEMLAPYIPMDDDFQL 44
RESULT 24
AAO23490
ID AAO23490 standard; peptide; 54 AA.
XX AC AAO23490;
XX DT 12-FEB-2004 (first entry)
XX DE Murine HIF-1alpha protein N-TAD region fragment (residues 531-584).
XX KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
XX KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
XX KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
XX KW N-TAD.
XX OS Mus sp.
XX PN WO2003074560-A2.
XX PD 12-SEP-2003.

PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 PI Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.
 XX
 XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 XX Example 11; Fig 27; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;
 Query Match 63.5%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 25 DLDLEMLAPYIPMDDDFQL 43
 |||||
 RESULT 26
 ID AAO23528
 AC AAO23528
 XX AAO23528;
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 XX (ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.
 XX

PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 XX Example 11; Fig 27; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;
 Query Match 63.5%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 25 DLDLEMLAPYIPMDDDFQL 43
 |||||
 RESULT 27
 ID AAO23529
 AC AAO23529 standard; peptide; 54 AA.
 XX
 XX AAO23529;
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 XX (ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.
 XX
 CC New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 XX Example 11; Fig 27; 96pp; English.

CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aqueora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis and glycolysis
XX
SQ Sequence 116 AA;
Query Match 63.5%; Score 101; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 31 DLDLEMLAPYIPMDDDFQL 49
RESULT 29
AAAY94633
ID AAY94633 standard; protein; 288 AA.
AC AAY94633;
XX
XX 15-AUG-2000 (first entry)
DE HIF-1alpha variant protein sequence HIF-1alpha/526-813.
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX Homo sapiens.
OS
XX WO200029437-A1.
FN
XX 25-MAY-2000.
PD
XX 11-NOV-1999; 99WO-SE002053.
PF
XX 13-NOV-1998; 98SE-00003891.
PR
XX (PHAA) PHARMACIA & UPJOHN AB.
PA
XX Berkenstam A, Poellinger L;
PI
XX WPI; 2000-399715/34.
DR
XX Human hypoxia-inducible factor alpha variants for identifying compounds
XX that modulate its functional domain and regulate genes involved in
XX angiogenesis, erythropoiesis.
XX Claim 13; Page 77-78; 87pp; English.
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX multi-step process which includes hypoxia-dependent nuclear import and
XX activation of the transactivation domain. The HIF-1alpha consists of a
XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX nuclear localization sequence located at amino acids 718-584, a
XX transactivator domain (N-TAD) located between amino acids 531 and 584,
XX and a second transactivator domain (C-TAD) located between 813 and 826.
XX The invention relates to isolated variants of HIF-1alpha, such as that
XX represented by the present sequence. The variants are useful for
XX identifying compounds capable of modulating the function of a functional
XX domain of human HIF-1alpha. The method comprises contacting a candidate
XX compound with a cell expressing a HIF-1alpha variant conjugated to a
XX molecular probe. The localization of the probe can be detected in the
XX cell. The Aqueora victoria green fluorescent protein can be used as the
XX molecular probe. The compounds are useful for the regulation of HIF-
XX 1alpha target genes, such as those involved in the regulation of
XX angiogenesis, erythropoiesis and glycolysis
XX

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
XX that has (a) an altered transactivation capacity and improved stability
XX at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
XX pharmaceutical composition are useful for increasing angiogenesis,
XX interfering with a normal response to reoxygenation following hypoxia, or
XX treating a condition associated with HIF-1alpha underexpression in a
XX cell, a group of cells, or an organism, e.g. ischaemia, diabetic
XX retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
XX stroke. The proteins and pharmaceutical compositions are also useful for
XX mimicking the hypoxic response or artificially inducing a hypoxic
XX response in a cell, group of cells, or organism, inducing vascular
XX formation or vascular development in a cell or a group of cells,
XX increasing angiogenic activity in a cell, or influencing erythropoietin
XX production, metabolism, or an inflammatory response in a cell, a group of
XX cells, or an organism. Sequences AAO23518-30 represent mutant fragments
XX within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;
Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 25 DLDLEMLAPYIPMDDDFQL 43
RESULT 28
AAAY94632
ID AAY94632 standard; protein; 116 AA.
AC AAY94632;
XX
XX 15-AUG-2000 (first entry)
DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX Homo sapiens.
OS
XX WO200029437-A1.
FN
XX 25-MAY-2000.
PD
XX 11-NOV-1999; 99WO-SE002053.
PF
XX 13-NOV-1998; 98SE-00003891.
PR
XX (PHAA) PHARMACIA & UPJOHN AB.
PA
XX Berkenstam A, Poellinger L;
PI
XX WPI; 2000-399715/34.
DR
XX Human hypoxia-inducible factor alpha variants for identifying compounds
XX that modulate its functional domain and regulate genes involved in
XX angiogenesis, erythropoiesis.
XX Claim 13; Page 76-77; 87pp; English.
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX multi-step process which includes hypoxia-dependent nuclear import and
XX activation of the transactivation domain. The HIF-1alpha consists of a
XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX nuclear localization sequence located at amino acids 718-584, a
XX transactivator domain (N-TAD) located between amino acids 531 and 584,
XX and a second transactivator domain (C-TAD) located between 813 and 826.
XX

CC molecular probe. The compounds are useful for the regulation of HIF-
CC lalpa target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis

XX Sequence 288 AA;

Query Match 63.5%; Score 101; DB 3; Length 288;

Best Local Similarity 100.0%; Pred. No. 5.5e-06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 30

AAV94634

ID AAY94634 standard; protein; 301 AA.

XX AAY94634;

XX 15-AUG-2000 (first entry)

XX HIF-lalpa variant protein sequence HIF-lalpa/526-826.

XX Hypoxia-inducible factor lalpa; HIF-lalpa; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.

XX Claim 13; Page 78-79; 87pp; English.

XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -lalpa amino acid sequence. The mechanism of action of HIF-lalpa is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-lalpa consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-lalpa between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-lalpa, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-lalpa. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-lalpa variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC lalpa target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis

XX Sequence 301 AA;

Query Match 63.5%; Score 101; DB 3; Length 301;

Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 31

AAV94631

ID AAY94631 standard; protein; 311 AA.

XX AAY94631;

XX 15-AUG-2000 (first entry)

XX HIF-lalpa variant protein sequence HIF-lalpa/331-641.

XX Hypoxia-inducible factor lalpa; HIF-lalpa; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.

XX Claim 13; Page 74-75; 87pp; English.

XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -lalpa amino acid sequence. The mechanism of action of HIF-lalpa is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-lalpa consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-lalpa between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-lalpa, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-lalpa. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-lalpa variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC lalpa target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis

XX Sequence 311 AA;

Query Match 63.5%; Score 101; DB 3; Length 311;

Best Local Similarity 100.0%; Pred. No. 5.9e-06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 226 DLDLEMLAPYIPMDDDFQL 244

```

RESULT 33
AAB68415
ID AAB68415 standard; protein; 444 AA.
XX
AC AAB68415;
XX
XX 23-JUL-2001 (first entry)
XX
XX Amino acid sequence of tTAK-hH104.
XX
XX Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
KW autoimmune disease; hH104; tTAK.
XX
XX Synthetic.
XX
XX WO200136616-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-FR003207.
XX
XX 18-NOV-1999; 99FR-00014513.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX
XX Beuzard Y, Payen E, Scherman D, Bettan M;
XX
XX WPI; 2001-343818/36.
XX
XX N-PSDB; AAF85323.
XX
XX New nucleic acid construct for controlling expression of target gene,
PT useful e.g. for treating cancer, is modulated by exogenous
PT pharmaceutical and oxygen partial pressure.
XX
XX Disclosure; Page 57-58; 60pp; French.
XX
XX The specification describes a nucleic acid construct bearing a system for
CC regulating the expression of a gene. The nucleic acid construct comprises
CC at least one sequence encoding a protein that regulates expression of at
CC least one gene of interest. The activity of this protein is modulated by
CC presence/absence of a pharmacological agent and the amount of protein
CC produced depends on the oxygen partial pressure. The constructs are used
CC to treat conditions associated with cellular hypoxia, especially anemia,
CC cancer and ischemia, specifically where the gene of interest encodes
CC erythropoietin (but many other suitable genes are listed, e.g. those
CC encoding single-chain antibodies for immunotherapy of infections or
CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
CC etc.). The present sequence is encoded by the open reading frame of tTAK-
CC hH104. The sequence contains a human hH104 fragment, inserted into the
CC BiWi1 site of tTAK. The sequence is used to produce constructs of the
CC invention.
XX
XX Sequence 444 AA;
XX
XX Query Match 63.5%; Score 101; DB 4; Length 444;
XX Best Local Similarity 100.0%; Pred. No. 8,7e-06;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
XX
XX 12 DLDLEMLAPYIPMDDDFQL 30
XX | | | | | | | | | | | | | |
XX 242 DLDLEMLAPYIPMDDDFQL 260
XX
XX RESULT 34
XX AD039390
XX ID AD039390 standard; protein; 466 AA.
XX
XX AD039390;
XX
XX

```

DT 15-JUL-2004 (first entry)
 XX Chimeric transactivator THV fragment #4.
 DE
 XX
 XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 XX
 XX Homo sapiens.
 OS
 XX US2004018606-A1.
 PN
 XX 29-JAN-2004.
 PD
 XX 30-APR-2003; 2003US-00425833.
 PF
 XX 30-APR-2002; 2002US-0376269P.
 PR
 XX (BOHL/) BOHL D.
 PA (HEAR/) HEARD M.
 XX
 XX Bohl D, Heard M;
 PI
 XX WPI; 2004-122040/12.
 DR N-PSDB; ADO39385.
 XX
 XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.
 XX
 XX Disclosure: Fig 6I; 28pp; English.
 PS
 XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer, anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
 CC transcription factor gene and VP16.
 XX
 XX Sequence 466 AA;
 SQ
 Query Match 63.5%; Score 101; DB 8; Length 466;
 Best Local Similarity 100.0%; Pred. No. 9.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 235 DLDLEMLAPYIPMDDDFQL 253
 RESULT 35
 ADO39387
 ID ADO39387 standard; protein; 538 AA.
 XX
 AC ADO39387;

XX 15-JUL-2004 (first entry)
 DT Chimeric transactivator THV fragment #1.
 DE
 XX
 XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 XX
 XX Homo sapiens.
 OS
 XX US2004018606-A1.
 PN
 XX 29-JAN-2004.
 PD
 XX 30-APR-2003; 2003US-00425833.
 PF
 XX 30-APR-2002; 2002US-0376269P.
 PR
 XX (BOHL/) BOHL D.
 PA (HEAR/) HEARD M.
 XX
 XX Bohl D, Heard M;
 PI
 XX WPI; 2004-122040/12.
 DR N-PSDB; ADO39382.
 XX
 XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.
 XX
 XX Disclosure: Fig 6F; 28pp; English.
 PS
 XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer, anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
 CC transcription factor gene and VP16.
 XX
 XX Sequence 538 AA;
 SQ
 Query Match 63.5%; Score 101; DB 8; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 364 DLDLEMLAPYIPMDDDFQL 382
 RESULT 36
 ABP41474
 ID ABP41474 standard; protein; 542 AA.
 XX

ABP41474;
22-AUG-2002 (first entry)
Human ovarian antigen HNORJ10, SEQ ID NO:2606.
Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.
Homo sapiens.
WO200200677-A1.
03-JAN-2002.
07-JUN-2001; 2001WO-US018569.
07-JUN-2000; 2000US-0209467P.
(HUMA-) HUMAN GENOME SCI INC.
Birse CE, Rosen CA;
WPI; 2002-147878/19.
N-PSDB; ABQ54551.
Isolated nucleic acid molecules encoding novel ovarian polypeptides,
useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
cancer), immune disorders, cardiovascular disorders and neurological
diseases.
Claim 11; SEQ ID NO 2606; 2922pp; English.
The invention relates to 2175 novel human ovarian antigens (ABP41054-
ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
encompasses polypeptides 90% identical and polynucleotides 95% identical
to the sequences of the invention. The invention additionally relates to
recombinant vectors and host cells comprising human ovarian antigen
polynucleotides, antibodies against human ovarian antigens, and the use
of ovarian antigen polynucleotides and polypeptides in diagnosing,
treating, prognosing or preventing various ovary and/or breast-related
disorders. Such conditions include ovarian cancer and breast cancer, and
metastatic tumours of ovarian or breast origin, reproductive system
disorders (e.g., infertility, disorders of pregnancy, anovulation,
polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
vaginitis), immune disorders (e.g., congenital and acquired
immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
blood-related disorders (e.g., anaemia), cardiovascular disorders,
respiratory disorders, neurological disorders, gastrointestinal disorders
and urinary system disorders. Ovarian antigen polypeptides and
polynucleotides may also be used in screening for compounds which
modulate ovarian antigen expression or activity. The polynucleotides may
further be used for gene therapy, chromosome mapping, in the
identification of individuals and in forensic analysis, and the
polypeptides may be used as food additives or to prepare antibodies
useful in disease diagnosis, drug targeting and phenotyping. The present
sequence represents a human ovarian antigen of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences
Sequence 542 AA;

Query Match 63.5%; Score 101; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAPYIPMDDDFQL 30
Db 272 DLDLEMLAPYIPMDDDFQL 290
RESULT 37
ADO39388
ID ADO39388 standard; protein; 595 AA.
XX ADO39388;
XX ADO39388;
XX 15-JUL-2004 (first entry)
XX Chimeric transactivator THV fragment #2.
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
XX normoxia; transcription factor degradation; anaemia; AIDS; cancer;
XX inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
XX tetracycline resistance; VP16.
XX Homo sapiens.
XX US2004018606-A1.
XX 29-JAN-2004.
XX 30-APR-2003; 2003US-00425833.
XX 30-APR-2002; 2002US-0376269P.
XX (BOHL/) BOHL D.
XX (HEAR/) HEARD M.
XX Bohl D, Heard M;
XX WPI; 2004-122040/12.
XX N-PSDB; ADO39383.
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
XX of a transcription factor susceptible to degradation under normoxia
XX conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
XX Disclosure; Fig 6G; 28pp; English.
XX The invention describes an isolated polynucleotide (1) which codes for a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions. Also described are: a chimeric transactivator comprising a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions; an isolated polynucleotide which codes for the chimeric
XX transactivator (1); a vector comprising the chimeric transactivator
XX polynucleotide (1); a composition comprising polynucleotide (2) and a
XX polynucleotide which contains a sequence that codes for a target gene and
XX a promoter which is regulated by the chimeric transactivator coded; a
XX method of expressing a target gene in a subject, comprising administering
XX the composition of (4); a method of increasing the number of red blood
XX cells in a subject, comprising administering the composition of (4) to
XX the subject; and a method of increasing the number of blood vessels in
XX the subject, comprising administering the composition of (4) to the subject.
XX The methods and compositions of the present invention are useful for
XX treating anaemia associated with AIDS or cancer, anaemia from
XX inflammatory origin and haemoglobinopathies. This is the amino acid
XX sequence of a fragment of a chimeric transactivator comprising regions of
XX the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
XX transcription factor gene and VP16.
XX Sequence 595 AA;

Query Match 63.5%; Score 101; DB 8; Length 595;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 38
 AAY94630
 ID AAY94630 standard; protein; 613 AA.
 XX
 AC AAY94630;
 DT
 DT 15-AUG-2000 (first entry)
 XX
 DE HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.
 XX
 KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200029437-A1.
 XX
 XX 25-MAY-2000.
 XX
 XX 11-NOV-1999; 99WO-SE002053.
 XX
 XX 13-NOV-1998; 98SE-00003891.
 XX
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX
 XX Berkenstam A, Poellinger L;
 XX WPI; 2000-399715/34.
 XX
 XX Human hypoxia-inducible factor alpha variants for identifying compounds
 XX that modulate its functional domain and regulate genes involved in
 XX angiogenesis, erythropoiesis.
 XX
 PS Claim 13; Page 72-74; 87pp; English.
 XX
 XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 XX multi-step process which includes hypoxia-dependent nuclear import and
 XX activation of the transactivation domain. The HIF-1alpha consists of a
 XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 XX nuclear localization sequence located at amino acids 718-584, a
 XX transactivator domain (N-TAD) located between amino acids 531 and 584,
 XX and a second transactivator domain (C-TAD) located between 813 and 826.
 XX The invention relates to isolated variants of HIF-1alpha, such as that
 XX represented by the present sequence. The variants are useful for
 XX identifying compounds capable of modulating the function of a functional
 XX domain of human HIF-1alpha. The method comprises contacting a candidate
 XX compound with a cell expressing a HIF-1alpha variant conjugated to a
 XX molecular probe. The localization of the probe can be detected in the
 XX cell. The Aequorea victoria green fluorescent protein can be used as the
 XX molecular probe. The compounds are useful for the regulation of HIF-
 XX 1alpha target genes, such as those involved in the regulation of
 XX angiogenesis, erythropoiesis and glycolysis
 XX
 XX Sequence 613 AA;

Query Match 63.5%; Score 101; DB 3; Length 613;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 39
 AAU77614
 ID AAU77614 standard; protein; 613 AA.
 XX
 AC AAU77614;
 XX
 XX 05-JUN-2002 (first entry)
 XX
 DE Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
 XX
 KW Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
 KW transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
 KW circulatory disorder; cancer; hypertension; demyelinating disorder;
 KW angiogenesis; sarcoidosis; hepatitis; hepatitis-caused inflammation;
 KW chronic ulceration; neovascularisation; arterial hypervascularisation;
 KW bullous skin disease; vasculitis; dermatomyositis; polymyositis; mutant;
 KW mitein; Y565G.
 XX
 XX Homo sapiens.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 177..178
 XX /note= "Residues 178-390 of the wild-type HIF-1 have been
 XX deleted"
 XX
 XX WO2000212326-A2.
 XX
 XX 14-FEB-2002.
 XX
 XX 07-AUG-2001; 2001WO-IB001775.
 XX
 XX 07-AUG-2000; 2000US-0223480P.
 XX
 XX (ASPE-) ASPERA PHARM AB.
 XX
 XX Poellinger L, Pereira T, Ruas J;
 XX WPI; 2002-257466/30.
 XX
 XX New polypeptides comprising hypoxia-inducible factor-1 with alterations
 XX of the transactivation domain, useful treating ischemic conditions, e.g.
 XX brain infarction, heart infarction or circulatory disorder.
 XX
 XX Example 5; Page; 80pp; English.

The invention relates to a polypeptide comprising hypoxia-inducible factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or C-TAD). Also included are nucleic acids encoding the altered proteins, a vector comprising the nucleic acid, a host cell transformed with the vector, methods for producing the protein or its functional fragment or an isolated degradation box, a method of screening for an agent that modulates N-TAD function and antagonists, agonists, modulators and HIF-1 peptide fragments useful for modulating HIF-1 function or the function of proteins that interact with it. The isolated polypeptides and their fragments with altered residues are useful in methods for treating diseases. The disease is an ischaemic condition, e.g. brain infarction, heart infarction or circulatory disorder. The disease may also be cancer, hypertension, demyelinating disorders, diffuse proliferative glomerulonephritis, toxoplasmosis caused retinochoroiditis, HIV (human immunodeficiency virus) caused T4 angioneurosis, HIV-caused Kaposi's sarcoma, hepatitis-caused inflammation, hepatitis-caused angioneurosis, chronic ulceration, proliferative retinopathy, retina haemangioblastomas, neovascularisation, arterial hypervascularisation, sarcoidosis, bullous skin disease, vasculitis with angiogenesis, dermatomyositis with angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis, juvenile osteoarthritis, polyarthritides, aneurysm or atheroma. The present sequence represents HIF-1 mutant delta 178-390. Note: The present sequence is not shown in the specification but was created by the indexer using the information in example 5 and the HIF sequence appearing as

CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 632 AA;
Query Match 63.5%; Score 101; DB 8; Length 632;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 235 DLDLEMLAPYIPMDDDFQL 253
RESULT 41
AAY94629
ID AAY94629 standard; protein; 652 AA.
XX
AC AAY94629;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/1-652.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SB002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
PI WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 15; Page 69-70; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transcription domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis and glycolysis
XX
SQ Sequence 652 AA;
Query Match 63.5%; Score 101; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

CC AAU77602
XX
SQ Sequence 613 AA;
Query Match 63.5%; Score 101; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 343 DLDLEMLAPYIPMDDDFQL 361
RESULT 40
ADO39391
ID ADO39391 standard; protein; 632 AA.
XX
AC ADO39391;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #5.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
PI WPI; 2004-122040/12.
XX
DR N-PSDB; ADO39386.
XX
PS New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
XX of a transcription factor susceptible to degradation under normoxia
XX conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
XX
PS Disclosure; Fig 6J; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC a subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 42
 AAY84167
 ID AAY84167 standard; protein; 669 AA.
 XX
 AC AAY84167;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX
 KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 KW ischemic tissue damage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200010578-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US019416.
 XX
 PR 25-AUG-1998; 98US-00148547.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Semenza GL;
 XX
 DR WPI; 2000-246493/21.
 XX
 PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 PT treating hypoxia or ischemia-related tissue damage.
 XX
 PS Claim 1; Page; 96pp; English.
 XX
 CC The present sequence represents a variant of hypoxia-inducible factor
 CC (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
 CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
 CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
 CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
 CC which residues 551 and 552 are not serine and threonine, respectively.
 CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
 CC expression of a hypoxia inducible gene in a cell. They is also useful for
 CC providing constitutive expression of a hypoxia inducible factor in a
 CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided
 XX
 SQ Sequence 669 AA;

Query Match 63.5%; Score 101; DB 3; Length 669;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 Db 399 DLDLEMLAPYIPMDDDFQL 417

RESULT 43

AAY84166
 ID AAY84166 standard; protein; 697 AA.
 XX
 AC AAY84166;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX
 KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 KW ischemic tissue damage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 422 /note= "this residue is optionally not Ser, and is
 FT preferably Gly"
 FT Misc-difference 423 /note= "this residue is optionally not Thr, and is
 FT preferably Ala"
 FT
 XX
 PN WO200010578-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US019416.
 XX
 PR 25-AUG-1998; 98US-00148547.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Semenza GL;
 XX
 DR WPI; 2000-246493/21.
 XX
 PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 PT treating hypoxia or ischemia-related tissue damage.
 XX
 PS Claim 1; Page; 96pp; English.
 XX
 CC The present sequence represents a variant of hypoxia-inducible factor
 CC (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type
 CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
 CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
 CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
 CC which residues 551 and 552 are not serine and threonine, respectively.
 CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
 CC expression of a hypoxia inducible gene in a cell. They is also useful for
 CC providing constitutive expression of a hypoxia inducible factor in a
 CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided
 XX
 SQ Sequence 697 AA;

Query Match 63.5%; Score 101; DB 3; Length 697;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 Db 427 DLDLEMLAPYIPMDDDFQL 445

RESULT 44

XX 03-JUL-2000 (first entry)
XX A variant of human hypoxia inducible factor-1 alpha protein.
XX Human: hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 449
FT /note= "this residue is not Ser, and is preferably Gly"
FT Misc-difference 450
FT /note= "this residue is not Thr, and is preferably Ala"
XX
PN WO200010578-A1.
XX
XX 02-MAR-2000.
XX
XX 25-AUG-1999; 99WO-US019416.
XX
XX 25-AUG-1998; 98US-00148547.
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Semenza GL;
XX
XX WPI; 2000-246493/21.
XX
XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
XX Claim 1; Page; 96pp; English.
XX
XX The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 494-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They are also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
XX Sequence 724 AA;
XX
XX Query Match 63.5%; Score 101; DB 3; Length 724;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-05;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 DLDLEMLAPYIPMDDDFQL 30
XX |||||
XX 454 DLDLEMLAPYIPMDDDFQL 472
XX
XX
XX RESULT 47
XX ABR82375
XX ID ABR82375 standard; protein; 735 AA.
XX
XX ABR82375;
XX
XX 06-NOV-2003 (first entry)
XX

XX Hypoxia-inducible factor 1 (HIF-1) alpha variant sequence.
DE
XX
XX HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquilizer; vulnerary; cardiant; cerebroprotective; variant.
XX
OS Homo sapiens.
XX
XX WO2003057820-A2.
XX
XX PD 17-JUL-2003.
XX
XX 04-OCT-2002; 2002WO-US031699.
XX
XX 21-DEC-2001; 2001US-00032361.
XX
XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
XX Mcgrath K;
XX
XX WPI; 2003-645988/61.
XX
XX Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX
XX Disclosure; Page 5-6; 37pp; English.
XX
XX The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC a HIF-1 alpha variant sequence
XX
XX Sequence 735 AA;
XX
XX Query Match 63.5%; Score 101; DB 6; Length 735;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-05;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 DLDLEMLAPYIPMDDDFQL 30
XX |||||
XX 556 DLDLEMLAPYIPMDDDFQL 574
XX
XX
XX RESULT 48
XX ADN75066
XX ID ADN75066 standard; protein; 735 AA.
XX
XX AC ADN75066;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human hypoxia-inducible factor 1 alpha #2.
XX
XX human; antisense therapy; hypoxia-inducible factor 1 alpha;
KW hyperproliferative disorder.
XX
XX Homo sapiens.
XX
XX US2004101858-A1.
XX
XX PD 27-MAY-2004.
XX
XX 23-NOV-2002; 2002US-00304126.
XX
XX 23-NOV-2002; 2002US-00304126.
XX
XX (ISIS-) ISIS PHARM INC.
XX

XX PI Ward DT, Dobie KW;
 XX DR WPI; 2004-399686/37.
 XX DR N-PSDB; ADN74945.
 XX PT New compounds, particularly oligonucleotides targeted to a nucleic acid
 XX PT encoding hypoxia-inducible factor 1 alpha, useful for treating diseases
 XX PT associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative
 XX PT disorders.
 XX PS Disclosure; Page 57-59; 80pp; English.
 XX CC The invention relates to antisense oligonucleotides targeted to, and
 XX CC which specifically hybridize with, and inhibit expression of, a nucleic
 XX CC acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense
 XX CC oligonucleotides are useful for treating a disease or condition
 XX CC associated with hypoxia-inducible factor 1 alpha, such as a
 XX CC hyperproliferative disorder. They are also useful in research and
 XX CC diagnostics for modulating the expression of hypoxia-inducible factor 1
 XX CC alpha. The present sequence represents human hypoxia-inducible factor 1
 XX CC alpha #2.
 XX SQ Sequence 735 AA;
 Query Match 63.5%; Score 101; DB 8; Length 735;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 556 DLDLEMLAPYIPMDDDFQL 574
 RESULT 49
 AAY84170
 ID AAY84170 standard; protein; 749 AA.
 XX AC AAY84170;
 XX DT 03-JUL-2000 (first entry)
 XX DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 XX KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 XX KW ischemia related damage; angiogenesis; coronary artery disease;
 XX KW ischemic tissue damage.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 474 /note= "this residue is not Ser, and is preferably Gly"
 XX FT Misc-difference 475 /note= "this residue is not Thr, and is preferably Ala"
 XX FT
 XX XN WO200010578-A1.
 XX XX
 XX PD 02-MAR-2000.
 XX XX
 XX PF 25-AUG-1999; 99WO-US019416.
 XX XX
 XX PR 25-AUG-1998; 98US-00148547.
 XX XX
 XX PA (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PI Semenza GL;
 XX XX
 XX DR WPI; 2000-246493/21.
 XX PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for

PT treating hypoxia or ischemia-related tissue damage.
 XX Claim 1; Page; 96pp; English.
 XX CC The present sequence represents a variant of hypoxia-inducible factor
 XX CC (HIF)-1 alpha, comprising amino acids 1-391 and 469-826 of the wild type
 XX CC protein (see AAY9407). The HIF-1alpha variants are stable under hypoxic
 XX CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 XX CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
 XX CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
 XX CC which residues 551 and 552 are not serine and threonine, respectively.
 XX CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
 XX CC expression of a hypoxia inducible gene in a cell. They are also useful for
 XX CC providing constitutive expression of a hypoxia inducible factor in a
 XX CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 XX CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 XX CC therapy for inducing the level of angiogenesis in tissues of patients at
 XX CC risk of coronary artery disease or ischemic tissue damage. note: this
 XX CC sequence does not appear in the specification; it was created using
 XX CC information provided
 XX SQ Sequence 749 AA;
 Query Match 63.5%; Score 101; DB 3; Length 749;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 DB 479 DLDLEMLAPYIPMDDDFQL 497
 RESULT 50
 AAY94635
 ID AAY94635 standard; protein; 756 AA.
 XX AC AAY94635;
 XX DT 15-AUG-2000 (first entry)
 XX DE HIF-1alpha variant protein sequence HIF-1alpha/71-826.
 XX KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 XX KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX OS Homo sapiens.
 XX OS WO200029437-A1.
 XX XN
 XX PD 25-MAY-2000.
 XX XX
 XX PF 11-NOV-1999; 99WO-SE002053.
 XX XX
 XX PR 13-NOV-1998; 98SE-00003891.
 XX PA (PHAA) PHARMACIA & UPJOHN AB.
 XX XX
 XX PI Berkenstam A, Foellinger L;
 XX XX
 XX DR WPI; 2000-399715/34.
 XX XX
 XX PT Human hypoxia-inducible factor alpha variants for identifying compounds
 XX PT that modulate its functional domain and regulate genes involved in
 XX PT angiogenesis, erythropoiesis.
 XX XX
 XX PS Claim 20; Page 79-82; 87pp; English.
 XX CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 XX CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 XX CC multi-step process which includes hypoxia-dependent nuclear import and
 XX CC activation of the transactivation domain. The HIF-1alpha consists of a
 XX CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 XX CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal

CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of
 CC angiogenesis, erythropoiesis and glycolysis
 XX
 SQ Sequence 756 AA;

Query Match 63.5%; Score 101; DB 3; Length 756;
 Best Local Similarity 100.0%; Pred.No. 1.5e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDEMLAPYIPMDDDFQL 30
 |||||
 Db 486 DLDEMLAPYIPMDDDFQL 504

Search completed: February 9, 2005, 06:05:43
 Job time : 168.175 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 79.4737 Seconds
(without alignments)
193.301 Million cell updates/sec

Title: US-10-032-361-7

Perfect score: 159

Sequence: 1 YGRKRRRRRLDLEMLAPVPMDDDFQL 30

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	65.4	766	1 HIFA_ONCMY	Q98sw2 oncorhynchu
2	103	64.8	777	2 Q6EH14	Q6eh14 brachydanio
3	102	64.2	774	2 Q6STN7	Q6stn7 ctenopharyn
4	101	63.5	786	2 Q6SL11	Q6sl11 canis famil
5	101	63.5	802	2 Q6PI54	Q6pi54 xenopus lae
6	101	63.5	805	1 HIFA_XENLA	Q918a9 xenopus lae
7	101	63.5	811	1 HIFA_CHICK	Q9yib9 gallus gall
8	101	63.5	819	2 Q7YSE5	Q7yse5 oryctolagus
9	101	63.5	821	2 Q64F54	Q64f54 spermophilu
10	101	63.5	823	1 HIFA_BOVIN	Q9xta5 bos taurus
11	101	63.5	823	2 Q6IV47	Q6iv47 bos mutus g
12	101	63.5	824	2 Q6H8T3	Q6h8t3 spalax juda
13	101	63.5	825	1 HIFA_RAT	Q35800 rattus norv
14	101	63.5	826	1 HIFA_HUMAN	Q16665 homo sapien
15	101	63.5	836	1 HIFA_MOUSE	Q61221 mus musculu
16	87	54.7	630	2 Q9QX54	Q9qx54 mus musculu
17	87	54.7	632	2 Q6RXA1	Q6rxal homo sapien
18	87	54.7	643	2 Q6STN6	Q6stn6 ctenopharyn
19	87	54.7	648	2 Q9HAI2	Q9hai2 homo sapien
20	87	54.7	662	2 Q9Z2I5	Q9z2i5 mus musculu
21	87	54.7	667	2 Q9Y2N7	Q9y2n7 homo sapien
22	87	54.7	669	2 Q66K72	Q66k72 homo sapien
23	86	54.1	571	2 Q7T2E4	Q7tze4 brachydanio
24	86	54.1	626	2 Q6EGR9	Q6egr9 brachydanio
25	84.5	53.1	662	2 Q9JHS2	Q9jhs2 rattus norv
26	82.5	51.9	859	2 Q6QI12	Q6qi12 xenopus lae
27	80.5	50.6	835	2 Q696W2	Q696w2 ctenopharyn
28	80.5	50.6	862	2 Q6GL61	Q6gl61 xenopus tro
29	80.5	50.6	862	2 Q6GP97	Q6gp97 xenopus lae
30	80.5	50.6	873	2 Q9QGM4	Q9qgm4 fundulus he
31	80	50.3	632	2 Q96K34	Q96k34 homo sapien

32	76.5	48.1	163	2 Q6RYD1	Q6ryd1 sus scrofa
33	76.5	48.1	164	2 Q6RYD0	Q6ryd0 ovis aries
34	76.5	48.1	867	2 Q9W7C6	Q9w7c6 gallus gall
35	76.5	48.1	870	1 PAS1_HUMAN	Q99814 homo sapien
36	76.5	48.1	870	2 Q9XTA4	Q9xta4 bos taurus
37	76.5	48.1	870	2 Q9PTB3	Q9ptb3 coturnix co
38	76.5	48.1	874	1 PAS1_MOUSE	P97481 mus musculu
39	76.5	48.1	874	1 PAS1_RAT	Q9jhs1 rattus norv
40	76.5	48.1	874	2 Q6PEU2	Q6peu2 mus musculu
41	65	40.9	235	2 Q8QG15	Q8qgi5 fundulus he
42	64.5	40.6	72	2 Q6GX21	Q6gx21 human immun
43	62.5	39.3	71	2 Q7L939	Q7l939 human immun
44	62.5	39.3	71	2 Q7L945	Q7l945 human immun
45	62.5	39.3	99	2 Q8UT76	Q8ut76 human immun
46	62.5	39.3	101	2 Q9QCH6	Q9qch6 human immun
47	62.5	39.3	101	2 Q9QCY2	Q9qcy2 human immun
48	62	39.0	86	2 Q8ADC2	Q8adc2 human immun
49	61.5	38.7	72	2 Q59628	Q59628 human immun
50	61	38.4	72	2 P88699	P88699 human immun
51	60.5	38.1	420	2 Q9FJ04	Q9fj04 arabidopsis
52	59.5	37.4	101	2 Q8QDF8	Q8qdf8 human immun
53	59.5	37.4	101	2 Q994G0	Q994g0 human immun
54	59	37.1	86	2 Q8ADL8	Q8adl8 human immun
55	59	37.1	99	2 Q9Q2T6	Q9q2t6 human immun
56	59	37.1	101	2 Q8Q7Z3	Q8q7z3 human immun
57	59	37.1	101	2 Q7ZJEO	Q7zjeo human immun
58	59	37.1	685	2 Q9RTU7	Q9rtu7 deinococcus
59	59	37.1	881	1 DX54_HUMAN	DX54 human eapien
60	58.5	36.8	72	2 P901Z7	P901z7 human immun
61	58.5	36.8	72	2 Q6GXZ2	Q6gxz2 human immun
62	58.5	36.8	72	2 Q6GXZ3	Q6gxz3 human immun
63	58.5	36.8	72	2 Q6GXZ4	Q6gxz4 human immun
64	58.5	36.8	72	2 Q6GXZ6	Q6gxz6 human immun
65	58.5	36.8	101	2 O71264	O71264 human immun

ALIGNMENTS

RESULT 1	HIFA_ONCMY	STANDARD;	PRT;	766 AA.
ID	HIFA_ONCMY	STANDARD;	PRT;	766 AA.
AC	Q98SW2;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).			
GN	Name=HIF1A;			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;			
RX	Soitamo A.J., Rabergh C.M.I., Gassmann M., Sistonen L., Nikkmaa M.;			
RA	"Characterization of a hypoxia-inducible factor (HIF-1 alpha) from			
RT	rainbow trout: accumulation of protein occurs at normal venous oxygen			
RT	tension."			
RL	J. Biol. Chem. 276:19699-19705(2001).			
CC	-!- FUNCTION: Functions as a master transcriptional regulator of the			
CC	adaptive response to hypoxia. Binds to core DNA sequence 5'-			
CC	[AG]CTG-3' within the hypoxia response element (HRE) of target			
CC	gene promoters. Activation requires recruitment of transcriptional			
CC	coactivators (By similarity).			
CC	-!- SUBUNIT: Efficient DNA binding requires heterodimerization of an			
CC	alpha and a beta/ARNT subunit (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear			
CC	translocation in response to hypoxia (By similarity).			
CC	-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.			
CC	-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.			
CC	-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.			

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
or send an email to license@ebi.ac.uk).
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EMBL; AF304864; AAK30364.1; --
HSSP; Q16665; IH2K.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR Activator; DNA-binding; Nuclear protein; Repeat;
Transcription regulation.
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 82 159 PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 368 373 Poly-Glu.
SQ SEQUENCE 766 AA; 85049 MW; FC25A4984104DASB CRC64;

Query Match 65.4%; Score 104; DB 1; Length 766;
Best Local Similarity 87.0%; Pred. No. 4.4e-06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRRDLEMLAPYIPMDDDFQL 30
Db 547 QAMEDLLEMLAPYIPMDDDFQL 569

RESULT 2
Q6EH14 PRELIMINARY; PRT; 777 AA.
AC Q6EH14
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia inducible factor 1 alpha.
GN Name=hif1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY326951; AAQ91619.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIA1F1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 774 AA; 85741 MW; 15BD082F90C611C6 CRC64;

Query Match 64.2%; Score 102; DB 2; Length 774;
Best Local Similarity 87.0%; Pred. No. 8.7e-06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRRDLEMLAPYIPMDDDFQL 30
Db 543 QAIEDLLEMLAPYIPMDDDFQL 565

RESULT 4
Q6SLL1 PRELIMINARY; PRT; 786 AA.
AC Q6SLL1
DR Q6SLL1
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIA1F1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 777 AA; 85897 MW; A9AFE2D2732C7A33 CRC64;

Query Match 64.8%; Score 103; DB 2; Length 777;
Best Local Similarity 87.0%; Pred. No. 6.3e-06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRRDLEMLAPYIPMDDDFQL 30
Db 545 QPMEDLLEMLAPYIPMDDDFQL 567

RESULT 3
Q6STN7 PRELIMINARY; PRT; 774 AA.
AC Q6STN7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1alpha.
GN Name=hif-1alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY450269; AAR95697.2; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIA1F1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 774 AA; 85741 MW; 15BD082F90C611C6 CRC64;

Query Match 64.2%; Score 102; DB 2; Length 774;
Best Local Similarity 87.0%; Pred. No. 8.7e-06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRRDLEMLAPYIPMDDDFQL 30
Db 543 QAIEDLLEMLAPYIPMDDDFQL 565

RESULT 4
Q6SLL1 PRELIMINARY; PRT; 786 AA.
AC Q6SLL1
DR Q6SLL1
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha subunit (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Spee B., Penning L.C., Roelhuizen J.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY455802; AAK19225.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAC; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 FT NON_TER 1 1
 FT TER 786 786
 SQ SEQUENCE 786 AA; 88015 MW; C37A27C25C343CDC CRC64;
 Query Match 63.5%; Score 101; DB 2; Length 786;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 536 DLDLEMLAPYIPMDDDFQL 554
 RESULT 5
 Q6PI54 PRELIMINARY; PRT; 802 AA.
 AC Q6PI54;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hif1a-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitman E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC043769; AAH43769.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAC; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 802 AA; 90177 MW; 30A571277A9A5B1F CRC64;
 Query Match 63.5%; Score 101; DB 2; Length 802;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYIPMDDDFQL 30
 Db 550 DLDLEMLAPYIPMDDDFQL 568
 RESULT 6
 HIFA_XENLA
 ID HIFA_XENLA STANDARD; PRT; 805 AA.
 AC Q91BA9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=HIF1a;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kietzmann T.;
 RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
 RT 1 alpha homologue.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 adaptive response to hypoxia. Binds to core DNA sequence 5'-

[AG]CTGTG-3' within the hypoxia response element (HRE) of target gene promoters. Activation requires recruitment of transcriptional coactivators (By similarity).

-1- SUBUNIT: Efficient DNA binding requires heterodimerization of an alpha and a beta/ARNT subunit (By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear translocation in response to hypoxia (By similarity).

-1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

-1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

-1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; AJ277829; CAB96628.1; --
HSP; Q16665; IH2K.
InterPro; IPR001092; HLH basic.
InterPro; IPR001321; HypoxindF1A.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR01080; HYPOXIAF1A.
PROSITE; PS50112; PAS; 2.
Activator; DNA-binding; Nuclear protein; Repeat;
Transcription regulation.
DNA BIND 17 30 Basic motif.
DOMAIN 31 71 Helix-loop-helix motif.
PAS 1.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Clausen I., Kietz S., Fischer B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY273790; AAP43517.1; -.
DR HSSP; Q16665; 1H2K.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 819 AA; 91284 MW; E11B4PBF7D4F6C7C CRC64;

Query Match 63.5%; Score 101; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 9
Q64F54
ID Q64F54 PRELIMINARY; PRT; 821 AA.
AC Q64F54;
DT 25-OCT-2004 (TrEMBLrel. 28, Created).
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypoxia-inducible factor 1 alpha subunit.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Morin P. Jr., Storey K.B.;
RT "Cloning and expression of HIF-1 from the hibernating ground squirrel,
RT Sperophilus tridecemlineatus.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY713478; AAU14021.1; -.
SQ SEQUENCE 821 AA; 92028 MW; 4C96BD0355CCCE06 CRC64;

Query Match 63.5%; Score 101; DB 2; Length 821;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 10
HIFA_BOVIN
ID HIFA_BOVIN STANDARD; PRT; 823 AA.
AC Q9XTA5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Artery;
RA MEDLINE=92525430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA Hara S., Kobayashi C., Imura N.;
RT "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF) -
RT 1alpha and -2alpha of bovine arterial endothelial cells.";
RL Biochim. Biophys. Acta 1445:237-243 (1999).
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -!- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-564.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -!- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC nitrosylated in vivo (By similarity).
CC -!- PTM: Acetylation of Lys-532 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -!- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB018398; BAA78675.1; -.
CC HSSP; Q16665; 1L8C.
CC InterPro; IPR001092; HLH_basic.
CC InterPro; IPR001321; Hypoxindf1A.

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DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 KW Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
 KW Phosphorylation; Repeat; S-nitrosylation; Transcription regulation;
 FT DOMAIN 718 721 Nuclear localization signal (Potential).
 FT DNA_BIND 17 30 Basic motif.
 FT DOMAIN 31 71 Helix-loop-helix motif.
 FT DOMAIN 85 158 PAS 1.
 FT DOMAIN 228 298 PAS 2.
 FT DOMAIN 302 345 PAC.
 FT DOMAIN 401 600 ODD.
 FT DOMAIN 531 575 NTAD.
 FT DOMAIN 576 782 ID.
 FT DOMAIN 783 823 CTAD.
 FT DOMAIN 715 718 Nuclear localization signal (Potential).
 FT MOD_RES 90 90 S-nitrosocysteine (Potential).
 FT MOD_RES 139 139 S-nitrosocysteine (Potential).
 FT MOD_RES 173 173 S-nitrosocysteine (Potential).
 FT MOD_RES 194 194 S-nitrosocysteine (Potential).
 FT MOD_RES 210 210 S-nitrosocysteine (Potential).
 FT MOD_RES 219 219 S-nitrosocysteine (Potential).
 FT MOD_RES 224 224 S-nitrosocysteine (Potential).
 FT MOD_RES 255 255 S-nitrosocysteine (Potential).
 FT MOD_RES 334 334 S-nitrosocysteine (Potential).
 FT MOD_RES 337 337 S-nitrosocysteine (Potential).
 FT MOD_RES 359 359 S-nitrosocysteine (Potential).
 FT MOD_RES 402 402 Hydroxyproline (By similarity).
 FT MOD_RES 520 520 S-nitrosocysteine (Potential).
 FT MOD_RES 532 532 N6-acetylllysine (By similarity).
 FT MOD_RES 564 564 Hydroxyproline (By similarity).
 FT MOD_RES 755 755 S-nitrosocysteine (Potential).
 FT MOD_RES 777 777 S-nitrosocysteine (Potential).
 FT MOD_RES 797 797 S-nitrosocysteine (Potential).
 FT MOD_RES 800 800 3-hydroxyasparagine (By similarity).
 SQ SEQUENCE 823 AA; 92127 MW; 126745467A61B1A1 CRC64;

Query Match 63.5%; Score 101; DB 1; Length 823;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
 Q61V47 PRELIMINARY; PRT; 823 AA.
 AC Q61V47;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypoxia inducible factor-1a.
 GN Name=HIF-1A;
 OS Bos mutus grunniens (Yak).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=30521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dolt K.S., Qadar Pasha M.A.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AY621118; AAT39520.1; --
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 823 AA; 92128 MW; A6E388E4FEA15705 CRC64;
 Query Match 63.5%; Score 101; DB 2; Length 823;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
 |||||
 Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 12
 Q6H8T3 PRELIMINARY; PRT; 824 AA.
 AC Q6H8T3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypoxia inducible factor 1 alpha.
 GN Name=hif-1a;
 OS Spalax judaei (Blind subterranean mole rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
 OC Spalax.
 OC NCBI_TaxID=134510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shams I., Avivi A., Nevo E.;
 RT "Hypoxic stress tolerance of the subterranean mole rat: Expression of
 erythropoietin and hypoxia-inducible factor-1a.";
 RL Nucleic Acids Res. 0:0-0(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shams I., Avivi A., Eviatar N.;
 RT "Hypoxic stress tolerance of the blind subterranean mole rat:
 expression of erythropoietin and hypoxia-inducible factor 1 alpha.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9698-9703(2004).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AJ715791; CAG29396.1; --
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.

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DR PRINTS; PR01080; HYPOXIAIF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE .824 AA; 92161 MW; 33A1DDC3593CBFF CRC64;

Query Match      63.5%; Score 101; DB 2; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 13
HIFA_RAT
ID HIFA_RAT STANDARD; PRT; 825 AA.
AC O35800; Q9WTU9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=Hif1a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Hepatocytes;
RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
RT "Perivenous expression of the mRNA of the three hypoxia-inducible
RL factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.;"
RL Biochem. J. 354:531-537(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=21417706; PubMed=11526200;
RA Zou A.-P., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
RT "Oxygen-dependent expression of hypoxia-inducible factor-lalpha in
RL renal medullary cells of rats.;"
RL Physiol. Genomics 6:159-168(2001).
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TA2-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
CC seen in the renal medulla than in the cortex. Expressed also in
CC the perivenous zone of the liver.
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory

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domain (ID) (By similarity).
-1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
The hydroxylated prolines promote interaction with VHL, initiating
rapid ubiquitination and subsequent proteasomal degradation. Under
hypoxia, proline hydroxylation is impaired and ubiquitination is
attenuated, resulting in stabilization (By similarity).
-1- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
abrogating interaction with CREBBP and EP300 and preventing
transcriptional activation (By similarity).
-1- PTM: S-nitrosylated. All free thiol groups are subjected to S-
nitrosylation in vitro, however not all thiol groups seem to be
nitrosylated in vivo (By similarity).
-1- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
and stimulates subsequent proteasomal degradation (By similarity).
-1- PTM: Phosphorylation is required for DNA binding (By similarity).
-1- SIMILARITY: Contains 1 basic helix-loop-helix (BHLH) domain.
-1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
-1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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or send an email to license@isb-sib.ch).
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CC EMBL; Y09507; CAA70701.1; -.
CC EMBL; AF057308; AAD24413.1; -.
CC HSSP; Q16665; IL8C.
CC TRANSFAC; T05461; -.
CC InterPro; IPR001092; HLH basic.
CC InterPro; IPR001321; Hypoxindf1A.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC Pfam; PF00010; HLH; 1.
CC Pfam; PF00785; PAC; 1.
CC Pfam; PF00989; PAS; 2.
CC PRINTS; PR01080; HYPOXIAIF1A.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00091; PAS; 2.
CC PROSITE; PS50888; HLH; 1.
CC PROSITE; PS50112; PAS; 2.
KW Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 85 158 PAS 1.
FT DOMAIN 228 298 PAS 2.
FT DOMAIN 302 345 PAC.
FT DOMAIN 401 602 ODD.
FT DOMAIN 530 574 NTAD.
FT DOMAIN 575 784 ID.
FT DOMAIN 717 720 Nuclear localization signal (Potential).
FT DOMAIN 785 825 CTAD.
FT MOD_RES 90 90 S-nitrosocysteine (Potential).
FT MOD_RES 139 139 S-nitrosocysteine (Potential).
FT MOD_RES 173 173 S-nitrosocysteine (Potential).
FT MOD_RES 194 194 S-nitrosocysteine (Potential).
FT MOD_RES 210 210 S-nitrosocysteine (Potential).
FT MOD_RES 219 219 S-nitrosocysteine (Potential).
FT MOD_RES 224 224 S-nitrosocysteine (Potential).
FT MOD_RES 255 255 S-nitrosocysteine (Potential).
FT MOD_RES 334 334 S-nitrosocysteine (Potential).
FT MOD_RES 337 337 S-nitrosocysteine (Potential).
FT MOD_RES 385 385 S-nitrosocysteine (Potential).
FT MOD_RES 402 402 Hydroxyproline (By similarity).
FT MOD_RES 519 519 S-nitrosocysteine (Potential).
FT MOD_RES 531 531 N6-acetyllysine (By similarity).

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FT MOD_RES 563 Hydroxyproline (By similarity).
FT MOD_RES 779 S-nitrosocysteine (Potential).
FT MOD_RES 799 S-nitrosocysteine (Potential).
FT MOD_RES 802 3-hydroxyasparagine (By similarity).
FT CONFLICT 12 K -> NR (in Ref. 2).
FT CONFLICT 74 D -> G (in Ref. 2).
FT CONFLICT 96 P -> L (in Ref. 2).
FT CONFLICT 329 D -> N (in Ref. 2).
FT CONFLICT 613 ATATAT -> TATA (in Ref. 2).
FT CONFLICT 708 R -> K (in Ref. 2).
SQ SEQUENCE 825 AA; 92319 MW; C4109A57F38667E9 CRC64;

Query Match 63 %; Score 101; DB 1; Length 825;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYPMDDDFQL 30
DB 555 DLDLEMLAPYPMDDDFQL 573

RESULT 14
HIFA HUMAN
ID HIFA HUMAN STANDARD; PRT; 826 AA.
AC Q16655; O96PT9; O9UPB1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE interacting protein) (Member of PAS protein 1) (MOP1).
GN Name=HIF1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
RX MEDLINE=95296340; PubMed=7539918;
RA Wang G.L., Jiang B.H., Rue E.A., Semenza G.L.;
RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT heterodimer regulated by cellular O2 tension.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway.";
RL J. Biol. Chem. 272:8581-8593 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99000835; PubMed=9782081; DOI=10.1006/geno.1998.5416;
RA Iyer N.V., Leung S.W., Semenza G.L.;
RT "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
RT evolutionary conservation.";
RL Genomics 52:159-165 (1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Rupert J.L., Hochachka P.W.;
RT "HIF1A sequence in the Quechua, a high altitude population.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Glial tumor;
RA Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Liver;
RA Tanaka S., Sugimachi K.;

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RT "Hypoxia-inducible factor-1 alpha variant isolated from human liver
RT tissue.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Choriocarcinoma, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP TRANSACTIVATION DOMAINS NTAD AND CTAD.
RX MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
RA Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
RT "Transactivation and inhibitory domains of hypoxia-inducible factor
RT 1alpha. Modulation of transcriptional activity by oxygen tension.";
RL J. Biol. Chem. 272:19253-19260 (1997).
RN [9]
RP SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
RX MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
RA Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
RA Poellinger L.;
RT "Signal transduction in hypoxic cells: inducible nuclear translocation
RT and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
RT factor-1alpha.";
RL EMBO J. 17:6573-6586 (1998).
RN [10]
RP OXYGEN-DEPENDENT DEGRADATION DOMAIN.
RX MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
RA Huang L.E., Gu J., Schau M., Bunn H.F.;
RT "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
RT dependent degradation domain via the ubiquitin-proteasome pathway.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992 (1998).
RN [11]
RP TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP MUTAGENESIS OF CYS-800.
RX MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA Poellinger L., Fujii-Kuriyama Y.;
RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT in response to hypoxia: their stabilization and redox signal-induced
RT interaction with CBP/p300.";
RL EMBO J. 18:1905-1914 (1999).
RN [12]
RP INTERACTION WITH NCOAL1, NCOA2 AND APEX.
RX MEDLINE=20063199; PubMed=10594042;
RA Carrero P., Okamoto K., Coumalleau P., O'Brien S., Tanaka H.,
RA Poellinger L.;
RT "Redox-regulated recruitment of the transcriptional coactivators CREB-
RT binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
RL Mol. Cell. Biol. 20:402-415 (2000).
RN [13]
RP MUTAGENESIS OF SER-551 AND THR-552.
RX MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
RA Sutter C.H., Laughner E., Semenza G.L.;
RT "Hypoxia-inducible factor 1alpha protein expression is controlled by

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RT oxygen-regulated ubiquitination that is disrupted by deletions and
 RT missense mutations.";
 RA Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
 RN [14]
 RP UBIQUITINATION.
 RX MEDLINE=21214630; PubMed=11292861; DOI=10.1126/science.1059796;
 RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
 RA Gaskell S.J., von Kriegsheim A., Hebestreit H.F., Mukherji M.,
 RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
 RT "Targeting of HIF-1alpha to the von Hippel-Lindau ubiquitylation
 RT complex by O2-regulated prolyl hydroxylation.";
 RL Science 292:468-472(2001).
 RN [15]
 RP S-NITROSYLATION.
 RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
 RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
 RT "HIF-1 alpha protein as a target for S-nitrosation.";
 RL FEBS Lett. 535:106-112(2003).
 RN [16]
 RP ACETYLATION OF LYS-532.
 RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
 RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
 RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
 RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
 RT acetylation.";
 RL Cell 111:709-720(2002).
 RN [17]
 RP HYDROXYLATION OF ASN-803.
 RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
 RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
 RA Bruck R.K.;
 RT "FIR-1 is an asparaginyl hydroxylase enzyme that regulates the
 RT transcriptional activity of hypoxia-inducible factor.";
 RL Genes Dev. 16:1466-1471(2002).
 RN [18]
 RP HYDROXYLATION OF PRO-402 AND PRO-564.
 RX MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
 RA Bruck R.K., McKnight S.L.;
 RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
 RL Science 294:1337-1340(2001).
 RN [19]
 RP REVIEW.
 RX MEDLINE=20407247; PubMed=10950862;
 RA Semenza G.L.;
 RT "HIF-1 and human disease: one highly involved factor.";
 RL Genes Dev. 14:1983-1991(2000).
 RN [20]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=20539371; PubMed=11089639;
 RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
 RA Michiels C.;
 RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
 RT 1) and its consensus DNA sequence.";
 RL J. Biomol. Struct. Dyn. 18:169-179(2000).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
 RP HIF1AN.
 RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
 RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.P.,
 RA Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
 RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
 RT mechanism of oxidative modification of HIF-1 alpha.";
 RL J. Biol. Chem. 278:1802-1806(2003).
 RN [22]
 RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
 RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
 RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
 RA Wagner G., Eck M.J.;
 RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
 RT factor-1 alpha.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
 RN [23]
 RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.

RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
 RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
 RA Wright P.E.;
 RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular
 RT
 Query Match 63.5%; Score 101; DB 1; Length 826;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAPYPMDDDFQL 30
 DB 556 DLDLEMLAPYPMDDDFQL 574
 RESULT 15
 HIFA_MOUSE
 ID HIFA_MOUSE STANDARD; PRT; 836 AA.
 AC Q61221; O08741; O08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
 AC Q8R385; Q8CYA8;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
 DE interacting protein).
 GN Name=Hif1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Hepatocytes;
 RX MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
 RA Li H., Ko H.P., Whitlock J.P. Jr.;
 RT "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
 RT Roles of Arnt and Hif1alpha.";
 RL J. Biol. Chem. 271:21262-21267(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129/SvJ;
 RX MEDLINE=98034461; PubMed=9368100;
 RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
 RA Bradfield C.A.;
 RT "Molecular characterization of the murine Hif-1 alpha locus.";
 RL Gene Expr. 6:287-299(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=129/SvJ;
 RX MEDLINE=97354184; PubMed=9210478;
 RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
 RA Gassmann M.;
 RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
 RT organization, expression and characterization of an alternative first
 RT exon and 5' flanking sequence.";
 RL Eur. J. Biochem. 246:155-165(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon; Diencephalon, Embryo, and Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 13-822 FROM N.A. (ISOFORM 2).
RC TISSUE=Hepatocytes;
RX MEDLINE=96254028; PubMed=8660378; DOI=10.1006/bbr.1996.0845;
RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
RA "Nucleotide sequence, chromosomal assignment and mRNA expression of
RT mouse hypoxia-inducible factor-1 alpha";
RL Biochem. Biophys. Res. Commun. 223:54-59 (1996).
RN [7]
RP SEQUENCE OF 22-85 FROM N.A.
RC TISSUE=Hepatocytes;
RA O'Rourke J.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOAL or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOAL and CREBBP (By
CC similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOAL, NCOA2, APEX and HSP90 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61221-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q61221-2; Sequence=VSP_007739;
CC TISSUE SPECIFICITY: Ubiquitous.
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-577 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-577.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Asn-813 by HIF1AN, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC nitrosylated in vivo (By similarity).
CC -1- PTM: Acetylation of Lys-545 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (BHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U59496; AAC52730.1; --
CC EMBL; AF003695; AAC53455.1; --
CC EMBL; Y09085; CAA70306.1; JOINED.
CC EMBL; Y13656; CAA70306.1; JOINED.
CC EMBL; Y09085; CAA70305.1; --
CC EMBL; AF004155; AAC53461.1; --
CC EMBL; AF004141; AAC53461.1; JOINED.
CC EMBL; AF004142; AAC53461.1; JOINED.
CC EMBL; AF004143; AAC53461.1; JOINED.
CC EMBL; AF004144; AAC53461.1; JOINED.
CC EMBL; AF004145; AAC53461.1; JOINED.
CC EMBL; AF004146; AAC53461.1; JOINED.
CC EMBL; AF004147; AAC53461.1; JOINED.
CC EMBL; AF004148; AAC53461.1; JOINED.
CC EMBL; AF004149; AAC53461.1; JOINED.
CC EMBL; AF004150; AAC53461.1; JOINED.
CC EMBL; AF004151; AAC53461.1; JOINED.
CC EMBL; AF004152; AAC53461.1; JOINED.
CC EMBL; AF004153; AAC53461.1; JOINED.
CC EMBL; AF004154; AAC53461.1; JOINED.
CC EMBL; AF004157; BAC28578.1; --
CC EMBL; AK034087; BAC36320.1; --
CC EMBL; AK076395; BAC28305.1; --
CC EMBL; AK033471; BAC28305.1; --
CC EMBL; AK017853; BAC30975.1; --
CC EMBL; BC026139; AAH26139.1; --
CC EMBL; X95580; CAA64833.1; --
CC EMBL; X95002; CAA64458.1; --
CC PIR; JC4837; JC4837.
CC TRANSFAC; T04666; --
CC MGI; MGI:106918; Hif1a.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.

Query Match 63.5%; Score 101; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LDLEMLAPYIPMDDDFQL 30
    |||||
DB 569 LDLEMLAPYIPMDDDFQL 587

RESULT 16
Q9QX54 PRELIMINARY; PRT; 630 AA.
AC Q9QX54;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypoxia-inducible factor 3 alpha (Fragment).
GN Name=Hif3a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT "Cloning and Characterization of a Third Hypoxia Inducible Factor,
RT HIF3-alpha.";
RL J. Biol. Chem. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99054547; PubMed=9840812;
RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT "Molecular characterization and chromosomal localization of a third
RT alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL Gene Expr. 7:205-213(1998).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF079153; AAF21782.1; JOINED.
DR EMBL; AF079140; AAF21782.1; JOINED.
DR EMBL; AF079141; AAF21782.1; JOINED.
DR EMBL; AF079143; AAF21782.1; JOINED.
DR EMBL; AF079145; AAF21782.1; JOINED.
DR EMBL; AF079147; AAF21782.1; JOINED.
DR EMBL; AF079149; AAF21782.1; JOINED.
DR EMBL; AF079151; AAF21782.1; JOINED.
DR EMBL; AF079152; AAF21782.1; JOINED.
DR EMBL; AF079150; AAF21782.1; JOINED.
DR EMBL; AF079148; AAF21782.1; JOINED.
DR EMBL; AF079146; AAF21782.1; JOINED.
DR EMBL; AF079144; AAF21782.1; JOINED.
DR EMBL; AF079142; AAF21782.1; JOINED.
DR HSSP; Q99814; IP97.
DR MGD; MGI:1859778; Hif3a.
DR GO; GO:0005634; C:nucleus; IC.
DR GO; GO:0003700; F:transcription factor activity; IPI.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR InterPro; IPR001092; Nuc translocat.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR001610; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
FT NON_TER 630
SQ SEQUENCE 630 AA; 69623 MW; 828EB2CB486D45B6 CRC64;

Query Match 54.7%; Score 87; DB 2; Length 630;
Best Local Similarity 94.4%; Pred. No. 0.00098;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDDFQL 30
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DB 569 LDLEMLAPYIPMDDDFQL 587

RESULT 18
Q6STN6 PRELIMINARY; PRT; 643 AA.
AC Q6STN6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypoxia-inducible factor-4alpha.
GN Name=hif-4alpha;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR
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Db 480 LDLEMLAPYIPMDDDFQL 497
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RESULT 17
Q8WXAI PRELIMINARY; PRT; 632 AA.
ID Q8WXAI;
AC Q8WXAI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Inhibitory PAS domain protein.
GN Name=IPAS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng J.Q.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF463492; AAL69947.1; -.
DR HSSP; Q16665; ILQB.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 632 AA; 68963 MW; 9665B0AF3998F8EF CRC64;

Query Match 54.7%; Score 87; DB 2; Length 632;
Best Local Similarity 94.4%; Pred. No. 0.00099;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDDFQL 30
    |||||
DB 485 LDLEMLAPYIPMDDDFQL 502

RESULT 18
Q6STN6 PRELIMINARY; PRT; 643 AA.
AC Q6STN6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypoxia-inducible factor-4alpha.
GN Name=hif-4alpha;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
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DR InterPro; IPR000014; PAS; 2.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 643 AA; 72434 MW; D73C6DD10086C4D CRC64;

Query Match 54.7%; Score 87; DB 2; Length 643;
Best Local Similarity 63.0%; Pred. No. 0.001;
Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 KKRQRRLDLEMLAPYIPMDDDFOL 30
DB 487 KQSEAMDELDLMLAPYISMDDDFOL 513

RESULT 19
Q9HAI2 PRELIMINARY; PRT; 648 AA.
AC Q9HAI2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ11591.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwawana T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyaana H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai K., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK021653; BAB13865.1; -.
DR HSP; Q16665; 1LQB.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001610; PAS.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00989; PAS; 1.
DR SMART; SM00086; PAS; 1.

DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 648 AA; 69955 MW; EBEFC744BC3F148E CRC64;

Query Match 54.7%; Score 87; DB 2; Length 648;
Best Local Similarity 94.4%; Pred. No. 0.001;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDDFOL 30
DB 429 LDLEMLAPYISMDDDFOL 446

RESULT 20
Q9Z2I5 PRELIMINARY; PRT; 662 AA.
AC Q9Z2I5
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia inducible factor three alpha.
GN Name=Hif3a;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99054547; PubMed=9840812;
RA Gu Y.Z., Moran S.M., Hogenesch J.B., Watanabe L., Bradfield C.A.;
RT "Molecular characterization and chromosomal localization of a third
RT alpha-class hypoxia inducible factor subunit, HIF3alpha."
RL Gene Expr. 7:205-213(1998).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF060194; AAC72734.1; -.
DR HSP; Q99814; 1P97.
DR MGD; MGI:1859778; Hif3a.
DR GO; GO:0005634; C:nucleus; IC.
DR GO; GO:0003700; F:transcription factor activity; IPI.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAS; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 662 AA; 73012 MW; 58740A1B6993D3B5 CRC64;

Query Match 54.7%; Score 87; DB 2; Length 662;
Best Local Similarity 94.4%; Pred. No. 0.001;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDDFOL 30
DB 480 LDLEMLAPYISMDDDFOL 497

RESULT 21
Q9Y2N7 PRELIMINARY; PRT; 667 AA.
AC Q9Y2N7
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative homolog of hypoxia inducible factor three alpha (Hypoxia-
DE inducible factor-3 alpha).
GN Name=HIF-3a;
```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamberdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=21458277; PubMed=11573933; DOI=10.1006/bbrc.2001.5659;
 RA Hara S., Hamada J., Kobayashi C., Kondo Y., Imura N.;
 RT "Expression and characterization of hypoxia-inducible factor (HIF)-
 RT alpha in human kidney: suppression of HIF-mediated gene expression by
 RT HIF-3alpha";
 RL Biochem. Biophys. Res. Commun. 287:808-813(2001).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AC007193; AAD22668.1; -;
 DR EMBL; AB054067; BAB63689.1; -;
 DR PIR; JC7771; JC7771.
 DR HSP; Q16665; LLOB.
 DR Genew; HGNC:15825; HIF3A.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; Nucleotidyl transferase domain.
 DR InterPro; IPR001067; Nucleotidyl transferase domain.
 DR InterPro; IPR001610; PAC.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PRO0785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 667 AA; 72404 MW; 67B8794FF9DCCF4B CRC64;

Query Match 54.7%; Score 87; DB 2; Length 667;
 Best Local Similarity 94.4%; Pred. No. 0.001;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDFQL 30
 DB 483 LDLEMLAPYISMDDFQL 500

RESULT 22
 Q66K72
 ID Q66K72 PRELIMINARY; PRT; 669 AA.
 AC Q66K72
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE HIF3A protein.
 GN Name=HIF3A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC080551; AAB80551.1; -;
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001067; Nucleotidyl transferase domain.
 DR Pfam; PF00010; HLH; 1.
 DR PRINTS; PRO0785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 669 AA; 72460 MW; 7EF732A1691AE6D CRC64;

Query Match 54.7%; Score 87; DB 2; Length 669;
 Best Local Similarity 94.4%; Pred. No. 0.001;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAPYIPMDDFQL 30
 DB 485 LDLEMLAPYISMDDFQL 502

RESULT 23
 Q7T2E4
 ID Q7T2E4 PRELIMINARY; PRT; 571 AA.
 AC Q7T2E4
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein hif1a.
 GN Name=hif1a;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054582; AAH54582.1; -.
DR HSP; Q99814; 1P97.
DR ZFIN; ZDB-GENE-040426-1315; hif1a1.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
KW Hypothetical protein.
SQ SEQUENCE 571 AA; 63846 MW; 1BA8E4CC29F16672 CRC64;

Query Match 54.1%; Score 86; DB 2; Length 571;
Best Local Similarity 84.2%; Pred. No. 0.0012;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
Db 430 ELDLMLAPYISMDDDFQL 448

RESULT 24
Q6EGR9 PRELIMINARY; PRT; 626 AA.
AC Q6EGR9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hif3a.
GN Name=hif3a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY330295; AAQ94179.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR001067; Nuc_translocat.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.

RESULT 25
Q9JHS2 PRELIMINARY; PRT; 662 AA.
AC Q9JHS2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 3 alpha.
GN Name=hif-3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RL MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA Kletznann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
RT "Periveneous expression of the mRNA of the three hypoxia-inducible
RT factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL Biochem. J. 354:531-537(2001).
CC 1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ277827; CAB96611.1; -.
DR HSP; Q99814; 1P97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 662 AA; 72887 MW; AC9672E340544010 CRC64;

Query Match 53.1%; Score 84.5; DB 2; Length 662;
Best Local Similarity 52.8%; Pred. No. 0.0024;
Matches 19; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

Qy 4 KKRQRRLD-----DLEMLAPYIPMDDDFQL 30
Db 462 RKNKMTETDLDAQDPDTPDLEMLAPYISMDDDFQL 497

RESULT 26
Q6GQ12 PRELIMINARY; PRT; 859 AA.
AC Q6GQ12
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 626 AA; 70221 MW; EA12390DFECF90B9 CRC64;

Query Match 54.1%; Score 86; DB 2; Length 626;
Best Local Similarity 84.2%; Pred. No. 0.0014;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
Db 485 ELDLMLAPYISMDDDFQL 503

RESULT 25
Q9JHS2 PRELIMINARY; PRT; 662 AA.
AC Q9JHS2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 3 alpha.
GN Name=hif-3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RL MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA Kletznann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
RT "Periveneous expression of the mRNA of the three hypoxia-inducible
RT factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL Biochem. J. 354:531-537(2001).
CC 1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ277827; CAB96611.1; -.
DR HSP; Q99814; 1P97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 662 AA; 72887 MW; AC9672E340544010 CRC64;

Query Match 53.1%; Score 84.5; DB 2; Length 662;
Best Local Similarity 52.8%; Pred. No. 0.0024;
Matches 19; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

Qy 4 KKRQRRLD-----DLEMLAPYIPMDDDFQL 30
Db 462 RKNKMTETDLDAQDPDTPDLEMLAPYISMDDDFQL 497

RESULT 26
Q6GQ12 PRELIMINARY; PRT; 859 AA.
AC Q6GQ12
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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RESULT 27
Q696W2
ID Q696W2 PRELIMINARY; PRT; 835 AA.
AC
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypoxia-inducible factor 2 alpha.
GN Name:hif-2alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
ON [1]
RN
RP SEQUENCE FROM N.A.
RA Law S.H.W., Kong R.Y.C., Wu R.S.S.;
RT "Molecular characterization of hypoxia-inducible factor-2alpha (hif-2alpha) gene in grass carp.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
ENBL; AY577524; AAT76668.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; NucTranslocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 835 AA; 92830 MW; CAE59E9A AFC785FD CRC64;

Query Match 50.6%; Score 80.5; DB 2; Length 835;
Best Local Similarity 85.0%; Pred. No. 0.012; 1; Indels 1; Gaps:
Matches 17; Conservative 1; Mismatches 1;

QY 12 DLDLEMLAPYIPMD-DDFQL 30
||||| ||||||| |||||
DB 518 DLDLETLAPYIPMDGEFQL 537

RESULT 28
Q6GL61
ID Q6GL61 PRELIMINARY; PRT; 862 AA.
AC
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Epas1-prov protein.
GN Name=epas1-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
ON [1]
RN
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RT MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shemen C.M., Schuler G.D.

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC074648; AAH74648.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001067; NUC_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 862 AA; 97138 MW; C2976D62101531CE CRC64;
Query Match 50.6%; Score 80.5; DB 2; Length 862;
Best Local Similarity 85.0%; Pred. No. 0.012;
Matches 17; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAPYIPMD-DDFOL 30
DB 517 DLDLETLAPYIPMDGEDFQL 536
RESULT 29
Q6GP97
ID Q6GP97 PRELIMINARY; PRT; 862 AA.
AC Q6GP97;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MGC80589 protein.
GN Name=MGC80589;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC073244; AAH73244.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; NUC_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 862 AA; 97319 MW; 3AC8FB39032E9E60 CRC64;
Query Match 50.6%; Score 80.5; DB 2; Length 862;
Best Local Similarity 85.0%; Pred. No. 0.012;
Matches 17; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAPYIPMD-DDFOL 30
DB 518 DLDLETLAPYIPMDGEDFQL 537
RESULT 30
Q6QGM4
ID Q6QGM4 PRELIMINARY; PRT; 873 AA.
AC Q6QGM4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 2 alpha.
OS Fundulus heteroclitus (Killifish) (Mummichog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21329980; PubMed=11932946; DOI=10.1002/jez.10074;
 RA Powell W.H., Hahn M.E.;
 RT "Identification and functional characterization of Hypoxia-inducible
 RT factor 2alpha from the estuarine teleost, Fundulus heteroclitus;
 RT Interaction of HIF2a with two ARNT2 splice variants.";
 J. Exp. Zool. 294:117-29(2002).
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AF402782; AAL95711.1; --
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; NUC_translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 873 AA; 96437 MW; BA2CF40AB4BC7B0 CRC64;
 Query Match 50.6%; Score 80.5; DB 2; Length 873;
 Best Local Similarity 85.0%; Pred. No. 0.012;
 Matches 17; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 12 DLDLEMLAPYIPMD-DDFQL 30
 DB 541 DLDLETLAPYIPMDGDFQL 560
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 RESULT 31
 ID Q96K34 PRELIMINARY; PRT; 632 AA.
 AC Q96K34;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14819.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX PubMed=14702039; DOI=10.1038/ngl1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuma K., Sato K., Tanikawa M., Yamashita H.,
 RA Ninomiya K., Ishibashi T., Yamashita K., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
 RA Higashigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AK027725; BAB55324.1; --
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; NUC_translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 632 AA; 68933 MW; A19F1ED3D05E7A71 CRC64;
 Query Match 50.3%; Score 80; DB 2; Length 632;
 Best Local Similarity 88.9%; Pred. No. 0.01;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 13 LDLEMLAPYIPMDDDFQL 30
 DB 485 LDLEMLAPYISMGDDFQL 502
 ||||| ||||| ||||| |||||
 RESULT 32
 ID Q6RYD1 PRELIMINARY; PRT; 163 AA.
 AC Q6RYD1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Endothelial PAS domain protein 1 (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=99823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ing N.H., Balog C.J., Wolfskill R.L.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY485673; AAR37390.1; --
 FT NON_TER 1
 FT NON_TER 163
 SQ SEQUENCE 163 AA; 17207 MW; 679CDA9F183CCAD3 CRC64;
 Query Match 48.1%; Score 76.5; DB 2; Length 163;

Best Local Similarity 80.0%; Pred. No. 0.0068; Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQOL 30
Db 118 ELDLETLAPYIPMDGEDFQOL 137

RESULT 33
Q6RYD0 PRELIMINARY; PRT; 164 AA.

AC Q6RYD0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Endothelial PAS domain protein 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Ing N.H., Balog C.J., Wolfskill R.L.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485674; AAR37391.1; --
FT NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 17405 MW; 49DBB95BA3D6D826 CRC64;

Query Match 48.1%; Score 76.5; DB 2; Length 164;
Best Local Similarity 80.0%; Pred. No. 0.0069; Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQOL 30
Db 119 ELDLETLAPYIPMDGEDFQOL 138

RESULT 34
Q9W7C6 PRELIMINARY; PRT; 867 AA.

AC Q9W7C6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Endothelial PAS domain protein 1.
GN Name=EPAS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRATN=breed White Leghorn;
RX MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA Favier J., Kempf H., Corvol P., Gasc J.-M.,
RT "Cloning and expression pattern of EPAS1 in the chicken embryo.
Colocalization with tyrosine hydroxylase."
RL FEBS Lett. 462:19-24(1999).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF129813; AAD38358.1; --
DR HSP; Q99814; IP97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; bHLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PRO0785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 867 AA; 97133 MW; DE674A948DE11DCC CRC64;

Query Match 48.1%; Score 76.5; DB 2; Length 867;
Best Local Similarity 80.0%; Pred. No. 0.045; Matches 16; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQOL 30
Db 522 ELDLETLAPYIPMDGEDFQOL 541

RESULT 35
PAS1_HUMAN STANDARD; PRT; 870 AA.

AC Q99814; Q86VA2; Q99630;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2) (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (HLF).
DE (HIF-1 alpha-like factor) (HLF).
GN Name=EPAS1; Synonyms=HIF2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152468; PubMed=9000051;
RA Tian H., McKnight S.L., Russell D.W.;
RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor selectively expressed in endothelial cells."
RL Genes Dev. 11:72-82(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA pray-Grant M., Perdev G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS superfamily that interacts with components of the dioxin signaling pathway."
RL J. Biol. Chem. 272:8581-8593(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dergé J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP MUTAGENESIS OF CYS-844.
RX MEDLINE-99219869; PubMed-10202154; DOI=10.1093/emboj/18.7.1905;
RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA Poellinger L., Fujii-Kuriyama Y.;
RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
in response to hypoxia: their stabilization and redox signal-induced
interaction with CBP/p300.";
RL EMBO J. 18:1905-1914(1999).
CC -!- FUNCTION: Transcription factor involved in the induction of oxygen
regulated genes. Binds to core DNA sequence 5'-(AG)CGTG-3' within
the hypoxia response element (HRE) of target gene promoters.
CC Regulates the vascular endothelial growth factor (VEGF) expression
and seems to be implicated in the development of blood vessels and
the tubular system of lung. May also play a role in the formation
of the endothelium that gives rise to the blood brain barrier.
CC Potent activator of the Tie-2 tyrosine kinase expression.
CC Activation seems to require recruitment of transcriptional
coactivators such as CREBBP and probably EP300. Interaction with
CC redox regulatory protein APEX seems to activate CTAD.
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
similarity).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
in placenta, lung and heart. Selectively expressed in endothelial
cells.
CC -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
prolines promote interaction with VHL, initiating rapid
ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
attenuated, resulting in stabilization (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
preventing abrogating interaction with CREBBP and EP300 and
preventing transcriptional activation (By similarity).
CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; U01984; A041495.1; -;
CC EMBL; U51626; AAC51212.1; -;
CC EMBL; BC051338; AAH51338.1; -;
CC PDB; 1P97; NMR; A=237-350.
CC TRANSFAC; T02718; -;
CC Genew; HGNC:3374; EPAS1.
CC MIM; 603349; -;
CC GO; GO:0003705; F:RNA polymerase II transcription factor acti. . . ; TAS.
CC GO; GO:0003713; F:transcription coactivator activity; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC GO; GO:0006366; P:transcription from Pol II promoter; TAS.
CC InterPro; IPR001092; HLH basic.
CC InterPro; IPR001087; NucTranslocat.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC Pfam; PF00010; HLH; 1.
CC Pfam; PF00785; PAC; 1.
CC Pfam; PF00989; PAS; 1.
CC PRINTS; PR00785; NCTRNLOCATR.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
KW 3D-structure; Activator; Angiogenesis; Developmental protein;
KW DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW Transcription regulation.
FT DNA_BIND 15 27 Basic motif.
FT DOMAIN 28 68 Helix-loop-helix motif.
FT PAS 1. PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 496 542 NTAD.
FT DOMAIN 830 870 CTAD.
FT MOD_RES 405 405 Poly-Ser.
FT MOD_RES 531 531 Hydroxyproline (By similarity).
FT MOD_RES 840 840 Hydroxyproline (By similarity).
FT MOD_RES 847 847 Phosphothreonine (By similarity).
FT MOD_RES 844 844 3-hydroxyasparagine (By similarity).
FT MUTAGEN 844 844 C->S: Abolishes hypoxia-inducible
transcriptional activation of ctad.
FT CONFLICT 60 60 A -> E (in Ref. 1).
FT CONFLICT 539 539 D -> G (in Ref. 2).
FT CONFLICT 601 601 H -> R (in Ref. 2).
FT CONFLICT 693 693 D -> N (in Ref. 2).
FT CONFLICT 716 716 E -> K (in Ref. 2).
FT CONFLICT 722 722 L -> P (in Ref. 2).
FT CONFLICT 765 765 F -> L (in Ref. 2).
FT CONFLICT 769 769 P -> S (in Ref. 2).
FT CONFLICT 844 844 C -> R (in Ref. 2).
FT CONFLICT 847 847 N -> K (in Ref. 2).
SQ SEQUENCE 870 AA; 96458 MW; 4838989598234FC1 CRC64;
Query Match 48.1%; Score 76.5; DB 1; Length 870;
Best Local Similarity 80.0%; Pred. No. 0.046;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAPYIPMD-DDFQL 30
:|||||:|||||:|||||
Db 523 ELDLETLAPYIPMDGEDFQL 542
RESULT 36
Q9XTA4 PRELIMINARY; PRT; 870 AA.
AC Q9XTA4;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Endothelial PAS domain protein 1/hypoxia-inducible factor-2
DE alpha.
GN Name=EPAS1/HIF2 alpha;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Arterial;
RX MEDLINE-99255430; PubMed-10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA Hara S., Kobayashi C., Imura N.;
RT "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
1alpha and -2alpha of bovine arterial endothelial cells.";
RL Biochim. Biophys. Acta 1445:237-243(1999).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC EMBL; AB018399; BAA78676.1; -;
CC HSP; Q99814; 1P97.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0004871; F:signal transducer activity; IEA.
CC GO; GO:0003700; F:transcription factor activity; IEA.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC GO; GO:0007165; P:signal transduction; IEA.
CC InterPro; IPR001092; HLH_basic.

DR InterPro; IPR001067; Nuc_translocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR00785; NCTRNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS50888; HLH; 1.

DR PROSITE; PS50112; PAS; 2.

SQ SEQUENCE 870 AA; 96168 MW; FEC602E6012D7712 CRC64;

Query Match 48.1%; Score 76.5; DB 2; Length 870;

Best Local Similarity 80.0%; Pred. No. 0.046;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQL 30

DB 522 ELDETLPYIPMDGEDFQL 541

RESULT 37

Q9PTB3

ID Q9PTB3

AC Q9PTB3

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 26, Last annotation update)

DE Hypoxia-inducible factor 2 alpha.

OS Coturnix coturnix (Common quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Coturnix.

OX NCBI_TaxID=9091;

RN SEQUENCE FROM N.A.

RP MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;

RX Elvert G., Lanz S., Kappel A., Flamme I.,

RT "mRNA cloning and expression studies of the quail homolog of HIF-2

alpha.";

RL Mech. Dev. 87:193-197(1999).

CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AF212989; AAF21052.1; --

DR HSSP; Q99814; 1P97.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR001092; HLH basic.

DR InterPro; IPR001067; Nuc_translocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR00785; NCTRNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS50888; HLH; 1.

DR PROSITE; PS50112; PAS; 2.

SQ SEQUENCE 870 AA; 97803 MW; 086AC8CF1639D77C CRC64;

Query Match 48.1%; Score 76.5; DB 2; Length 870;

Best Local Similarity 80.0%; Pred. No. 0.046;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAPYIPMD-DDFQL 30

DB 522 ELDETLPYIPMDGEDFQL 541

RESULT 38

PASI_MOUSE

ID PASI_MOUSE

AC P97481; O08787; O55046;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2

alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (NHLF)

DE (HIF-related factor) (HRF).

GN Names=Epas1; Synonyms=Hif2a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

MEDLINE=97152468; PubMed=9000051;

Tian H., McKnight S.L., Russell D.W.,

RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor

selectively expressed in endothelial cells.";

RL Genes Dev. 11:72-82(1997).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6; TISSUE=Hypothalamus, and Skeletal muscle;

RX MEDLINE=97272213; PubMed=9113973; DOI=10.1073/pnas.94.9.4273;

Ena M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,

Fujii-Kuriyama Y.,

RT "A novel bHLH-PAS factor with close sequence similarity to hypoxia-

inducible factor 1alpha regulates the VEGF expression and is

potentially involved in lung and vascular development.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).

[3]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain capillary;

MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;

Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,

Risau W.,

RT "HRF, a putative basic helix-loop-helix-PAS-domain transcription

factor is closely related to hypoxia-inducible factor-1 alpha and

developmentally expressed in blood vessels.";

RL Mech. Dev. 63:51-60(1997).

[4]

RN SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.

RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;

Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,

Bruick R.K.,

RT "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the

transcriptional activity of hypoxia-inducible factor.";

RL Genes Dev. 16:1466-1471(2002).

[5]

RN INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS

OF THR-844.

RX MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;

Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.,

RT "The transcriptional activation function of the HIF-like factor

requires phosphorylation at a conserved threonine.";

RL J. Biol. Chem. 277:23508-23514(2002).

[6]

RN HYDROXYLATION OF ASN-851.

RX MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;

Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.,

RT "Asparagine hydroxylation of the HIF transactivation domain a hypoxic

switch.";

RL Science 295:858-861(2002).

CC -1- FUNCTION: Transcription factor involved in the induction of oxygen

regulated genes. Binds to core DNA sequence 5'-(AG)CGTG-3' within

the hypoxia response element (HRE) of target gene promoters.

CC Regulates the vascular endothelial growth factor (VEGF) expression

and seems to be implicated in the development of blood vessels and

the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier.
 Potent activator of the Tie-2 tyrosine kinase expression.
 Activation requires recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 -!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP.
 -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels in lung, followed by heart, kidney, brain and liver. Predominantly expressed in endothelial cells. Also found in smooth muscle cells of the uterus, neurons, and brown adipose tissue. High expression in embryonic choroid plexus and kidney glomeruli.
 -!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost exclusively seen in endothelial cells of the intersegmental blood vessels separating the somites, the atrial and ventricular chambers of the heart, and the dorsal aorta. High expression also occurs in extra-embryonic membranes. In the developing brain of day 13 embryo, endothelial cells of the highly vascularized choroid plexus contain high levels of EPAS1.
 -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).
 -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation.
 -!- PTM: Phosphorylated on multiple sites in the CTAD.
 -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; U81983; AAB41496.1; -
 EMBL; D89787; BAA20130.1; -
 EMBL; AF045160; AAC12871.1; -
 HSSP; Q16685; 1H2K.
 DR TRANSFAC; T02719; -
 DR MGD; MGI:109169; Epas1.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; Nuc_translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRFAMs; TIGR00229; sensory_box; 2.
 DR PROSITE; PS50888; HLH; FALSE_NEG.
 DR PROSITE; PS50112; PAS; 2.
 KW Activator; Angiogenesis; Developmental protein;
 KW Direct protein sequencing; DNA-binding; Hydroxylation;
 KW Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
 FT DNA_BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 CTAD.
 FT DOMAIN 834 874

FT	DOMAIN	471	479	Poly-Ser.
FT	MOD_RES	405	405	Hydroxyproline (By similarity).
FT	MOD_RES	530	530	Hydroxyproline (By similarity).
FT	MOD_RES	844	844	Phosphothreonine.
FT	MOD_RES	851	851	3-hydroxyasparagine.
FT	MUTAGEN	530	530	P->A: Confers transcriptional activity at normoxia; when associated with A-851.
FT	MUTAGEN	844	844	T->A: Decreases interaction with CREBBP.
FT	MUTAGEN	851	851	N->A: Confers transcriptional activity at normoxia; when associated with A-530.
FT	CONFLICT	25	25	C->S (in Ref. 2).
FT	CONFLICT	191	191	K->R (in Ref. 1).
FT	CONFLICT	439	440	VS->AA (in Ref. 3).
FT	CONFLICT	463	463	D->G (in Ref. 3).
FT	CONFLICT	654	654	G->V (in Ref. 2).
FT	CONFLICT	663	663	A->P (in Ref. 2).
FT	CONFLICT	669	669	S->W (in Ref. 1).
FT	CONFLICT	673	673	P->L (in Ref. 1).
FT	CONFLICT	678	678	P->L (in Ref. 1).
FT	CONFLICT	725	725	D->E (in Ref. 3).
FT	CONFLICT	731	731	P->L (in Ref. 3).
FT	CONFLICT	762	762	A->G (in Ref. 3).
FT	CONFLICT	786	786	P->L (in Ref. 3).
FT	CONFLICT	791	791	S->F (in Ref. 3).
FT	CONFLICT	794	794	S->N (in Ref. 3).
SQ	SEQUENCE	874 AA;	96712 MW;	A6FFA490AE43640C CRC64;

Query Match 48.1%; Score 76.5; DB 1; Length 874;
 Best Local Similarity 80.0%; Pred. No. 0.046; 1; Gaps 1;
 Matches 16; Conservative 2; Mismatches 1; Indels 1;
 QY 12 LDLEMLAPYIPMD-DDFQL 30
 :|||||:|||||:|||||
 Db 522 ELDETLAPYIPMDGEFQL 541

RESULT 39
 PAS1_RAT STANDARD; PRT; 874 AA.
 AC Q9JHS1;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha).
 GN Name=Epas1; Synonyms=Hif2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivenous expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 CC -!- FUNCTION: Transcription factor involved in the induction of oxygen regulated genes. Binds to core DNA sequence 5'-(AG)CTGG-3' within the hypoxia response element (HRE) of target gene promoters.
 CC Regulates the vascular endothelial growth factor (VEGF) expression and seems to be implicated in the development of blood vessels and the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier.
 CC Potent activator of the Tie-2 tyrosine kinase expression.
 CC Activation seems to require recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).

-!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).

-!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation (By similarity).

-!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).

-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; AJ277828; CAB96612.1; --
HSSP; Q16665; 1H2X.
InterPro; IPR001092; HLH basic.
InterPro; IPR001067; Nuc translocat.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAC.
Pfam; PF00010; HLH; 1.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR00785; NCTRNLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRfam; TIGR00229; sensory box; 2.
PROSITE; PS00888; HLH; FALSE_NEG.
PROSITE; PS0112; PAS; 2.
KW Activator; Angiogenesis; Developmental protein; DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW Transcription regulation.
FT DNA_BIND 15 27
FT DOMAIN 28 68
FT DOMAIN 84 154
FT DOMAIN 230 300
FT DOMAIN 304 347
FT DOMAIN 495 541
FT DOMAIN 834 874
FT DOMAIN 474 479
FT MOD_RES 405 405 Hydroxyproline (By similarity).
FT MOD_RES 530 530 Hydroxyproline (By similarity).
FT MOD_RES 844 844 Phosphothreonine (By similarity).
FT MOD_RES 851 851 3-hydroxyasparagine (By similarity).
SQ SEQUENCE 874 AA; 96718 MW; A1FF08EB24369796 CRC64;

Query Match 48.1%; Score 76.5; DB 1; Length 874;
Best Local Similarity 80.0%; Pred. No. 0.046; 1; Indels 1; Gaps 1;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDEMLAPYIPMD-DDFQL 30
:|||||:|||||:|||||
Db 522 ELDETLAPYIPMDGEDFQL 541

RESULT 40
Q6PEU2 PRELIMINARY; PRT; 874 AA.

AC Q6PEU2 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Endothelial PAS domain protein 1.
GN Name=Epsal;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Moore H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC057870; AAH57870.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 874 AA; 96636 MW; 2E6D7603A678EACE CRC64;

Query Match 48.1%; Score 76.5; DB 2; Length 874;
Best Local Similarity 80.0%; Pred. No. 0.046; 1; Indels 1; Gaps 1;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDEMLAPYIPMD-DDFQL 30
:|||||:|||||:|||||
Db 522 ELDETLAPYIPMDGEDFQL 541

RESULT 41
Q8QGI5 PRELIMINARY; PRT; 235 AA.

AC Q8QGI5 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 24, Last annotation update)
DE Hypoxia-inducible factor alpha-like protein (Fragment).
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 OX NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
 RA Powell W.H., Hahn M.E.;
 RT "Identification and functional characterization of hypoxia-inducible
 factor 2alpha from the estuarine teleost, Fundulus heteroclitus;
 interaction of HIF-2alpha with two ARNT2 splice variants.";
 RL J. Exp. Zool. 294:17-29(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Oleksiak M.F., Kellell K.J., Crawford D.L., Hahn M.E., Powell W.H.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF433668; AM12473.1; -;
 DR HSSP; G99814; IP97.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001610; PAC.
 DR SMART; SM00086; PAC; 1.
 FT NON_TER 1 235
 FT NON_TER 235
 SQ SEQUENCE 235 AA; 25400 MW; AE7A7C5D15827351 CRC64;
 Query Match 40.9%; Score 65; DB 2; Length 235;
 Best Local Similarity 80.0%; Pred. No. 0.46;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 14 DLEMLAPYIPMDDDF 28
 Db :|||||
 221 ELEMVAPYISMDDDF 235
 RESULT 42
 Q6GXZ1 PRELIMINARY; PRT; 72 AA.
 AC Q6GXZ1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Tat protein (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eric L., Kumar R., Hill M.D., Costas S., Chaudhary S., Tirado G.,
 RA Yamamura Y., Kumar A.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 trans-activating responsive sequence (TAR) RNA element and
 activates transcription initiation and/or elongation from the LTR
 promoter (By similarity).
 CC EMBL; AY620859; AAT48062.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription;
 Transcription regulation.
 FT NON_TER 72 72
 SQ SEQUENCE 72 AA; 8397 MW; 9D83E7DB3486EC2B CRC64;
 Query Match 40.6%; Score 64.5; DB 2; Length 72;
 Best Local Similarity 53.3%; Pred. No. 0.14;

Matches 16; Conservative 0; Mismatches 7; Indels 7; Gaps 1;
 QY 1 YGRKKRRQRRRLDLEMLAPYIPMDDDFQL 30
 Db :|||||
 47 YGRKKRRQRRR-----APRDSQDDQVSL 69
 RESULT 43
 Q71939 PRELIMINARY; PRT; 71 AA.
 AC Q71939;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Michael N.L.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 trans-activating responsive sequence (TAR) RNA element and
 activates transcription initiation and/or elongation from the LTR
 promoter (By similarity).
 CC EMBL; U24453; AAA79589.1; -;
 DR HSSP; P12506; ITBC.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PR00055; HIVTATDOMAIN.
 KW Activator; Nuclear protein; RNA-binding; Transcription;
 Transcription regulation.
 FT NON_TER 71 71
 SQ SEQUENCE 71 AA; 8307 MW; A3EFC2840AFF2A50 CRC64;
 Query Match 39.3%; Score 62.5; DB 2; Length 71;
 Best Local Similarity 58.3%; Pred. No. 0.27;
 Matches 14; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
 QY 1 YGRKKRRQRRR-DLDLEMLAPYIP 23
 Db :|||||
 47 YGRKKRRQRRRAPQDSQTYQAYLP 70
 RESULT 44
 Q71945 PRELIMINARY; PRT; 71 AA.
 AC Q71945;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Michael N.L.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 trans-activating responsive sequence (TAR) RNA element and
 activates transcription initiation and/or elongation from the LTR
 promoter (By similarity).

Qy


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CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; AF361876; AAK94259.1; -.
DR HSSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 101 AA; 11534 MW; 54592B65F004E284 CRC64;

Query Match 39.3%; Score 62.5; DB 2; Length 101;
Best Local Similarity 55.2%; Pred. NO. 0.41;
Matches 16; Conservative 1; Mismatches 9; Gaps 2;

QY 1 YGKRRRRRRRLDLEMLAPYIPMDDDFQ 29
DB 47 YGKRRRRRRR-----AP--PSGEDHQ 66

RESULT 48
Q8ADC2 PRELIMINARY; PRT; 86 AA.
AC Q8ADC2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tat protein.
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22375625; PubMed=12487816; DOI=10.1089/08922202320886325;
RA Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
RA Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA McCutchan F.E.;
RT "Among 46 near full length HIV type 1 genome sequences from Rakai
RT District, Uganda, subtype D and AD recombinants predominate.";
RL AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Harris M.E., Birx D.L., Robb M.L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Lutalo T.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Meehen M., Wawer M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
trans-activating responsive sequence (TAR) RNA element and
activates transcription initiation and/or elongation from the LTR
promoter (By similarity).
DR EMBL; AF484516; AAN73784.1; -.
DR HSSP; P04613; 1K5K.
DR GO; GO:0042025; C:host cell nucleus; IEA.
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DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 86 AA; 9905 MW; 01C995B36AE0161A CRC64;

Query Match 39.0%; Score 62; DB 2; Length 86;
Best Local Similarity 53.8%; Pred. NO. 0.4;
Matches 14; Conservative 0; Mismatches 2; Indels 10; Gaps 1;

QY 1 YGKRRRRRRRLDLEMLAPYIPMD 26
DB 47 YGKRRRRRRS-----PQDD 62

RESULT 49
Q69628 PRELIMINARY; PRT; 72 AA.
AC Q69628;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95264414; PubMed=7745674;
RA Diaz R.S., Sabino E.C., Mayer A., Mosley J.W., Busch M.P.;
RT "Dual human immunodeficiency virus type 1 infection and recombination
RT in a dually exposed transfusion recipient. The Transfusion Safety
RT Study Group.";
RL J. Virol. 69:3273-3281(1995).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
trans-activating responsive sequence (TAR) RNA element and
activates transcription initiation and/or elongation from the LTR
promoter (By similarity).
DR EMBL; U11191; AAA78877.1; -.
DR HSSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8428 MW; 4A00C4BF893D0E86 CRC64;

Query Match 38.7%; Score 61.5; DB 2; Length 72;
Best Local Similarity 65.2%; Pred. NO. 0.39;
Matches 15; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 YGKRRRRRRRLDLEMLAPYI 22
DB 47 YGKRRRRRRALKDSETHQAYL 69

RESULT 50
P88699 PRELIMINARY; PRT; 72 AA.
ID P88699
AC P88699;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
```

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Quinones-Mateu M.E.; Domingo E.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
DR EMBL; U80465; AAB39115.1; -.
DR HSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8342 MW; ED2C19A34DA4B591 CRC64;

Query Match 38.4%; Score 61; DB 2; Length 72;
Best Local Similarity 91.7%; Pred. No. 0.46;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKFKKRRRD 12
Db 47 YGKFKKRRRD 58
|||||:||||
|||||:||||

Search completed: February 9, 2005, 06:00:14
Job time : 81.4737 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 17.3684 Seconds
(without alignments)
166.193 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGRKKRRQRRRLDLEMLAPYIPMDDDFQL 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR 79: +
1: pir1: +
2: pir2: +
3: pir3: +
4: pir4: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	63.5	810	2 JC4837	hypoxia-inducible
2	101	63.5	811	2 JC7619	hypoxia-inducible
3	101	63.5	813	2 JC5809	hypoxia-inducible
4	101	63.5	826	2 I38972	hypoxia-inducible
5	87	54.7	667	2 JC7771	hypoxia-inducible
6	59	37.1	685	2 F75370	oligopeptidase A -
7	58	36.5	71	2 T09384	trans-activating t
8	58	36.5	72	1 TNLJH4	trans-activating t
9	58	36.5	86	1 TNLJZR	trans-activating t
10	58	36.5	86	2 JC5591	transactivator pro
11	58	36.5	86	2 A25700	trans-activating t
12	58	36.5	86	2 S54381	tat protein - huma
13	58	36.5	86	2 S33982	trans-activating t
14	58	36.5	87	2 T01665	tat protein - huma
15	58	36.5	95	1 TNLJ12	trans-activating t
16	58	36.5	101	1 E44001	trans-activating t
17	58	36.5	101	2 T09446	tat protein - huma
18	55	34.6	86	1 TNLJND	trans-activating t
19	54	34.0	713	2 S76766	hypothetical prote
20	54	34.0	1505	2 JC4851	hypoxia-inducible
21	51	32.1	220	1 B5AG58	virB5 protein prec
22	51	32.1	220	2 A13248	component of type
23	50	31.4	259	1 CTXLPB	corticotropin / li
24	50	31.4	260	1 CTXLPB	corticotropin / li
25	50	31.4	276	2 B38965	hypothetical prote
26	50	31.4	457	2 D83741	hypothetical prote
27	50	31.4	561	2 E70610	hypothetical prote
28	49.5	31.1	307	2 T01773	syntaxin homolog A
29	49	30.8	422	2 F64651	hypothetical prote

30	49	30.8	440	2	G71939	hypothetical prote
31	48.5	30.5	900	2	B70694	probable infB - My
32	48.5	30.5	924	2	F87103	initiation factor
33	48	30.2	107	2	A70966	hypothetical prote
34	48	30.2	232	2	D71218	hypothetical prote
35	48	30.2	233	2	D75185	hypothetical prote
36	48	30.2	561	2	S35637	high mobility grou
37	48	30.2	1021	2	A28199	H1R1 protein - yea
38	48	30.2	1021	2	A28199	Na+/K+-exchanging
39	48	30.2	1023	1	A24639	Na+/K+-exchanging
40	48	30.2	1023	1	A24639	Na+/K+-exchanging
41	48	30.2	1023	1	A24639	Na+/K+-exchanging
42	47.5	29.9	407	2	T37242	transforming growt
43	47.5	29.9	462	2	C85651	hypothetical prote
44	47.5	29.9	462	2	H90790	hypothetical prote
45	47.5	29.9	563	2	T20192	hypothetical prote
46	47.5	29.9	878	2	S74207	lipoygenase (EC 1
47	47	29.6	88	2	G64139	DNA-directed RNA p
48	47	29.6	124	2	B82444	hypothetical prote
49	47	29.6	279	2	A81971	lacto-N-neotetraos
50	47	29.6	344	2	I49585	CD2 antigen protei
51	47	29.6	344	2	B28967	T-cell surface gly
52	47	29.6	351	1	RWHUC2	T-cell surface gly
53	47	29.6	448	2	T03776	tat binding protei
54	47	29.6	540	2	A86020	hypothetical prote
55	47	29.6	540	2	A98174	hypothetical prote
56	47	29.6	540	2	S47708	hypothetical 61.2K
57	47	29.6	677	2	D87708	peptidyl-di-peptida
58	47	29.6	1021	1	S04630	Na+/K+-exchanging
59	47	29.6	1272	2	S26180	neurofascin - chic
60	47	29.6	1290	2	A56493	leucocyte common a
61	47	29.6	1298	2	I54367	X-linked nuclear p
62	47	29.6	1898	2	S46216	leukocyte antigen-
63	46.5	29.2	50	2	G84198	hypothetical prote
64	46.5	29.2	180	2	B97242	hypothetical prote
65	46.5	29.2	255	2	T46350	hypothetical prote

ALIGNMENTS

RESULT 1

JC4837 hypoxia-inducible factor 1 alpha - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4837
R:Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M.
Biochem. Biophys. Res. Commun. 223, 54-59, 1996
A:Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxi
A:Reference number: JC4837; MUID:96254028; PMID:8660378
A:Accession: JC4837
A:Molecule type: mRNA
A:Residues: 1-810 <WEN>
A:Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:gi430864; PIDN:CAA64833.1; PID:943;
C:Comment: This factor is involved in the oxygen-regulated transcription of several gen

A:Gene: Hif1alpha
A:Map position: 12
C:Keywords: transcription factor
F:5-58/Region: helix-loop-helix #status predicted

Query Match 63.5%; Score 101; DB 2; Length 810;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30
|||||
Db 543 DLDLEMLAPYIPMDDDFQL 561

RESULT 2

JC7619

Wed Feb 9 06:58:03 2005

hypoxia-inducible factor 1 alpha - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: J07619
R:Takahashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kingawa, K.; Harada, A.; Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
A>Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricle
A:Reference number: J07619; MUID:21134360; PMID:11237772
A:Contents: Embryonic ventricular myocytes
A:Accession: J07619
A:Molecule type: mRNA
A:Residues: 1-811 <TAK>
A:Cross-references: DBJ:AB013746
C:Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) family
of eukaryotic cells, and in redox stimuli.

C:Genetics:
A:Gene: hif-1alpha
C:Keywords: embryo; transcription factor
F:106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS>
F:249-299/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS>
F:762-811/Domain: conserved carboxy-terminal transactivation element #status predicted <PAS>
F:767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation

Query Match 63.5%; Score 101; DB 2; Length 811;

Best Local Similarity 100.0%; Pred. No. 7.2e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 554 DLDLEMLAPYIPMDDDFQL 572

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RESULT 3

J03909

hypoxia-inducible factor 1 alpha - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999

C:Accession: J03909

R:Ladoux, A.; Frelin, C.

Biochem. Biophys. Res. Commun. 240, 552-556, 1997

A>Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop helix/PAS domain

A:Reference number: J03909; MUID:98063274; PMID:9398602

A:Accession: J03909

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-813 <LAD>

C:Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator

as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, and

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

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F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

F:6-144/Region: basic helix-loop-helix #status predicted

Query Match 63.5%; Score 101; DB 2; Length 813;

Best Local Similarity 100.0%; Pred. No. 7.2e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAPYIPMDDDFQL 30

DB 543 DLDLEMLAPYIPMDDDFQL 561

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RESULT 4

I38972

hypoxia-inducible factor 1 alpha - human

N:Alternate names: ARNT interacting protein

C:Species: Homo sapiens (man)

C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: I38972; G01875

R:Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.

Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995

A>Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulated

A:Reference number: I38972; MUID:95296340; PMID:7539918

A:Accession: I38972

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-685 <WHI>

A:Residues: 1-826 <RBS>

A:Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:G881345; PIDN:AA050152.1; PID:G8813.

A>Note: parts of this sequence were confirmed by peptide sequencing

R:Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.

submitted to the EMBL Data Library, June 1995

A:Reference number: H00692

A:Accession: G01875

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-826 <HOG>

A:Cross-references: EMBL:U29165; NID:G1144012; PIDN:AA051210.1; PID:G1144013

C:Genetics:

A:Gene: GDB:HIF1A

A:Cross-references: GDB:512229

A:Map position: 14q21-14q24

C:Keywords: heterodimer

Query Match 63.5%; Score 101; DB 2; Length 826;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
A;Cross-references: UNIPROT:Q9RTU7; GB:AE002008; GB:AE000513; NID:G6459414; PIDN:AAF1121
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1659
A;Map position: 1
C;Superfamily: peptidyl-dipeptidase Dcp

Query Match 37.1%; Score 59; DB 2; Length 685;
Best Local Similarity 42.3%; Pred. No. 3.4;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAPYIPMD 26
DB 338 YWAEKQKQKDYDFDEALRPYALDN 363

RESULT 7
T09384
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09384
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir
J. Virol. 69, 4228-4236, 1995
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon
A;Reference number: Z16654; MUID:95287475; PMID:7769682
A;Accession: T09384
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-71 <MIC>
A;Cross-references: UNIPROT:Q71926; EMBL:U24451; NID:G829440; PIDN:AAA79576.1; PID:G8294
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription

Query Match 36.5%; Score 58; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 8
TNLJH4
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 02-Jul-1998
C;Accession: B25523
R;Deasi, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: B25523
A;Molecule type: DNA
A;Residues: 1-72 <DES>
A;Cross-references: GB:M13137; NID:G326460
A;Note: the GenBank entry ADRE3AA PID:G209908 differs from the published sequence in tra
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription regulation

Query Match 36.5%; Score 58; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57
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RESULT 9

TNLJZR

trans-activating transcription regulator - human immunodeficiency virus Zr-6
C;Species: human immunodeficiency virus Zr-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C26192
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; C

Gene 52, 71-82, 1987

A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot

A;Reference number: A26192; MUID:87248097; PMID:3036660

A;Accession: C26192

A;Molecule type: DNA

A;Residues: 1-86 <SRI>

A;Cross-references: UNIPROT:P04609; GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45377.1;

C;Genetics:

A;Gene: tat

A;Introns: 72/3

C;Superfamily: AIDS trans-activating transcription regulator

C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 36.5%; Score 58; DB 1; Length 86;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11

DB 47 YGRKKRRQRRR 57

RESULT 10

JC5591

transactivator protein - human immunodeficiency virus type 1

N;Alternate names: tat protein

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999

C;Accession: JC5591

R;Hoffmann, S.; Willbold, D.

Biochem. Biophys. Res. Commun. 235, 806-811, 1997

A;Title: A selection system to study protein-RNA interactions: Functional display of HIV

A;Reference number: JC5591; MUID:97350867; PMID:9207243

A;Accession: JC5591

A;Molecule type: protein

A;Residues: 1-86 <HO2>

C;Comment: This protein is a key regulatory protein in the viral replication cycle and

C;Superfamily: AIDS trans-activating transcription regulator

F;22-31/Region: cysteine-rich

Query Match 36.5%; Score 58; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11

DB 47 YGRKKRRQRRR 57

RESULT 11

A25700

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 09-Jul-2004

C;Accession: A25700

R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.

Science 229, 74-77, 1985

A;Reference number: A25700; MUID:85244627; PMID:2990041

A;Accession: A25700

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-86 <SOD>

A;Cross-references: UNIPROT:P04610

C;Superfamily: AIDS trans-activating transcription regulator

Wed Feb 9 06:58:03 2005

```
Query Match      36.5%; Score 58; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRRR 11
      |||||
Db      47 YGRKKRQRRR 57

RESULT 12
S54381
tat protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54381
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54381
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-86 <THE>
A:Cross-references: UNIPROT:P12506; EMBL:M22639; NID:G329377; PIDN:AAA45363.1; PID:G3293
C:Genetics:
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match      36.5%; Score 58; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRRR 11
      |||||
Db      47 YGRKKRQRRR 57

RESULT 13
S33982
trans-activating transcription regulator - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S33982; S26385; S19864
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33982
A:Molecule type: DNA
A:Residues: 1-86 <CAR>
A:Cross-references: UNIPROT:P04606; EMBL:Z11530; NID:G60192; PIDN:CAA77625.1; PID:G60196
R:Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Ezfle, H.; Summer-Sm
Nucleic Acids Res. 20, 5311-5320, 1992
A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c
A:Reference number: S26385; MUID:93065196; PMID:11437550
A:Accession: S26385
A:Molecule type: nucleic acid
A:Residues: 1-86 <SID>
A:Cross-references: EMBL:X64650; NID:G60144; PIDN:CAA45921.1; PID:G60145
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS, immunodeficiency

Query Match      36.5%; Score 58; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRRR 11
      |||||
Db      47 YGRKKRQRRR 57

RESULT 14
S54381
tat protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01665
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol.
A:Reference number: Z14389; MUID:86245056; PMID:2424612
A:Accession: T01665
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-87 <ALI>
A:Cross-references: UNIPROT:P04613; EMBL:K03456; NID:G60228; PIDN:CAA28015.1; PID:G602233
C:Genetics:
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match      36.5%; Score 58; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRRR 11
      |||||
Db      47 YGRKKRQRRR 57

RESULT 15
TNLJ12
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A04017
R:Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
A:Reference number: A94093; MUID:86177573; PMID:3008154
A:Accession: A04017
A:Molecule type: DNA
A:Residues: 1-95 <ARY>
A:Cross-references: UNIPROT:P04326
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match      36.5%; Score 58; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRQRRR 11
      |||||
Db      56 YGRKKRQRRR 66

RESULT 16
E44001
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain
N:Alternate names: tat protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: E44001
R:Li, Y.; Hu, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties o
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: E44001
A:Molecule type: DNA
A:Residues: 1-101 <LIY>
A:Cross-references: UNIPROT:P35965; GB:M93258
C:Genetics:
```

A:Gene: tat
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 36.5%; Score 58; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRQR 11
|||||
Db 47 YGKRRQR 57

RESULT 17

T09446

tat protein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09446
R: Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09446

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <PAN>

A:Cross-references: UNIPROT:Q75758; EMBL:U63632; NID:g1465777; PID:g1465783

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 36.5%; Score 58; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRQR 11
|||||
Db 47 YGKRRQR 57

RESULT 18

TNLJND

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: JQ0071

R: Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.; Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus type 1

A:Reference number: JQ0065; MUID:90034200; PMID:2806917

A:Accession: JQ0071

A:Molecule type: DNA

A:Residues: 1-86 <SPI>

A:Cross-references: UNIPROT:P18804; GB:M27323; NID:g328154; PIDN:AAA44866.1; PID:g328155

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription

Query Match 34.6%; Score 55; DB 1; Length 86;

Best Local Similarity 90.9%; Pred. No. 1.4;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKRRQR 11
|||||
Db 47 YGKRRQR 57

RESULT 19

S76766

virB5 protein precursor - Agrobacterium tumefaciens plasmid pTiC58
C:Species: Agrobacterium tumefaciens
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C:Accession: S12345; S11830; S10520

R: Shirasu, K.; Morel, P.; Kado, C.I. Mol. Microbiol. 4, 1153-1163, 1990

A:Title: Characterization of the virB operon of an Agrobacterium tumefaciens Ti plasmid

A:Reference number: S12341; MUID:91041724; PMID:2233252

A:Accession: S12345

A:Molecule type: DNA

hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76766

R: Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76766

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-713 <KAN>

A:Cross-references: UNIPROT:P74571; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA186

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Start codon: GTG

C:Superfamily: peptidyl-dipeptidase Dcp

Query Match 34.0%; Score 54; DB 2; Length 713;

Best Local Similarity 37.5%; Pred. No. 17;

Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 YGKRRQR 24
|||||
Db 357 YWSEQRQEFDFDAELRPYPPL 380

RESULT 20

JC4851

hypoxia-inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004

C:Accession: JC4851

R: Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T. Gene 172, 249-254, 1996

A:Title: The Drosophila melanogaster similar bHLH-PAS gene encodes a protein related to

A:Reference number: JC4851; MUID:96269413; PMID:8682312

A:Accession: JC4851

A:Molecule type: mRNA

A:Residues: 1-1505 <NAM>

A:Cross-references: UNIPROT:Q24167; GB:U43090; NID:g1174073; PIDN:AAC47303.1; PID:g1174

C:Genetics:

A:Gene: sima

A:Cross-references: FlyBase:FBgn0015542

A:Map position: 3

F:72-125/Region: helix-loop-helix #status predicted

F:171-433/Region: PAS domain #status predicted

F:506-635/Region: proline-rich

Query Match 34.0%; Score 54; DB 2; Length 1505;

Best Local Similarity 71.4%; Pred. No. 37;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 MLAPYIPMDDDPQL 30
|||||
Db 850 WRAPYIPDDDDMPL 863

RESULT 21

BSAG58

virB5 protein precursor - Agrobacterium tumefaciens plasmid pTiC58

C:Species: Agrobacterium tumefaciens

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C:Accession: S12345; S11830; S10520

R: Shirasu, K.; Morel, P.; Kado, C.I. Mol. Microbiol. 4, 1153-1163, 1990

A:Title: Characterization of the virB operon of an Agrobacterium tumefaciens Ti plasmid

A:Reference number: S12341; MUID:91041724; PMID:2233252

A:Accession: S12345

A:Molecule type: DNA

Wed Feb 9 06:58:03 2005

N;Contains: beta-endorphin; CLIP: corticotropin; lipotropin beta; melanotropin alpha; me
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01460; S03554; S03555; 151554
R;Martens, G.J.M.
Nucleic Acids Res. 14, 3791-3798, 1986
A;Title: Expression of two proopiomelanocortin genes in the pituitary gland of Xenopus l.
A;Reference number: A93621; MUID:86232619; PMID:3754961
A;Accession: A01460
A;Molecule type: mRNA
A;Residues: 1-259 <MAR1>
A;Cross-references: UNIPROT:P06298; GB:X03843; NID:G65004; PIDN:CAA27460.1; PID:G65005
R;Deen, P.M.T.; Buessemakers, M.J.G.; Terwel, D.; Roubos, E.W.; Martens, G.J.M.
Mol. Biol. Evol. 9, 483-494, 1992
A;Title: Comparative structural analysis of the transcriptionally active proopiomelanoco
A;Reference number: A42623; MUID:92261311; PMID:1584015
A;Accession: A42623
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-202, 'E', 204-259 <DEE>
A;Cross-references: GB:X59370; NID:G5931775; PIDN:CAA2013.2; PID:G5931776
R;Notte: this translation is not annotated in GenBank entry XLPOMCA, release 109
R;Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
FEBS Lett. 245, 215-218, 1989
A;Title: Particular processing of pro-opiomelanocortin in Xenopus laevis intermediate p
A;Reference number: S03554; MUID:89171310; PMID:2564347
A;Accession: S03554
A;Molecule type: protein
A;Residues: 140-149 <ROU1>
A;Note: amino end of melanotropin alpha, which is not acetylated in this preparation
A;Accession: S03555
A;Molecule type: protein
A;Residues: 'X', 211-225 <ROU2>
A;Note: amino end of melanotropin beta
R;Martens, G.J.M.; Civelli, O.; Herbert, E.
J. Biol. Chem. 260, 13685-13689, 1985
A;Title: Nucleotide sequence of cloned cDNA for pro-opiomelanocortin in the amphibian Xe
A;Reference number: 151554; MUID:86033833; PMID:3840481
A;Accession: 151554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'L', 58-259 <MAR2>
A;Cross-references: GB:M11346; NID:G214659; PIDN:AAA49932.1; PID:G214660
C;Genetics:
A;Introns: 43/3
C;Superfamily: corticotropin-lipotropin
C;Keywords: glycoprotein; hormone; neuropeptide; opioid peptide; pituitary
F;1-25/Domain: signal sequence #status predicted <SIG>
F;76-101/Product: melanotropin gamma #status predicted <WTG>
F;140-178/Product: corticotropin #status predicted <CTN>
F;140-154/Product: melanotropin alpha #status predicted <MTA>
F;157-178/Product: CLIP #status predicted <CLP>
F;181-259/Product: lipotropin beta #status predicted <LTB>
F;210-226/Product: melanotropin beta #status predicted <MTB>
F;229-259/Product: beta-endorphin #status predicted <BEF>
F;229-233/Product: Met-enkephalin #status predicted <MEN>
F;90/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 31.4%; Score 50; DB 1; Length 259;
Best Local Similarity 28.3%; Pred. No. 21;
Matches 13; Conservative 7; Mismatches 8; Indels 18; Gaps 1;
QY 2 GRKKR-----RRRRDLLEMLAPVPMDDFO 29
DB 153 GRKKRPKVYPNGVEESAESYPMELRRLSELDYPEIDLEDIE 198
RESULT 24
CTXLPB
corticotropin / lipotropin B precursor - African clawed frog
N;Alternate names: gamma-melanocyte stimulating hormone, POMC; pro-opiomelanocortin
N;Contains: beta-endorphin; CLIP: corticotropin; lipotropin beta; melanotropin alpha;
C;Species: Xenopus laevis (African clawed frog)
A;Residues: 1-220 <SHI>
A;Cross-references: UNIPROT:P17795; EMBL:J03320; NID:G154781; PIDN:AAA91595.1; PID:G1547
R;Rogowsky, P.M.; Powell, K.; Lin, T.S.; Morel, P.; Zyprian, E.M.; Steck,
Plasmid 23, 85-106, 1990
A;Title: Molecular characterization of the vir regulon of Agrobacterium tumefaciens: com
A;Reference number: S11825; MUID:90301800; PMID:2194232
A;Accession: S11830
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-220 <ROG>
A;Cross-references: EMBL:J03320; NID:G154781; PIDN:AAA91595.1; PID:G154787
R;Kulda, G.A.; de Vos, G.; Owen, J.; McCaffrey, G.; Zambryski, P.
Mol. Gen. Genet. 221, 256-266, 1990
A;Title: The virB operon of Agrobacterium tumefaciens pTiC58 encodes 11 open reading fra
A;Reference number: S10516; MUID:90318324; PMID:2370849
A;Accession: S10520
A;Molecule type: DNA
A;Residues: 1-220 <KUL>
A;Cross-references: EMBL:X53264; NID:G39152; PIDN:CAA37358.1; PID:G39157
C;Genetics:
A;Gene: virB5
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-220/Product: virB5 protein #status predicted <MAT>
Query Match 32.1%; Score 51; DB 1; Length 220;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 3 RKRRRRRLDLEMLAPVPM 24
DB 72 QKNQYPTSLDLEMLAPVPM 93
RESULT 22
AI3248
component of type IV secretion system [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3248
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KUR>
A;Cross-references: UNIPROT:P17795; GB:AE008690; PIDN:AAL46407.1; PID:G17744201; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: virB5
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein
Query Match 32.1%; Score 51; DB 2; Length 220;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 3 RKRRRRRLDLEMLAPVPM 24
DB 72 QKNQYPTSLDLEMLAPVPM 93
RESULT 23
CTXLPA
corticotropin / lipotropin A precursor - African clawed frog
N;Alternate names: POMC; proopiomelanocortin

C>Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004
 C/Accession: A01461; I51621; S18009; S03554; S03555; I51623; I51624; I51626; I51627; I51628; G.J.M.
 Nucleic Acids Res. 14, 3791-3798, 1986
 A>Title: Expression of two proopiomelanocortin genes in the pituitary gland of *Xenopus laevis*
 A/Reference number: A93621; MUID:86232619; PMID:3754961
 A/Accession: A01461
 A/Molecule type: mRNA
 A/Residues: 1-260 <MAR1>
 A/Cross-references: UNIPROT:P06299; GB:X03844; NID:G65011; PIDN:CAA27466.1; PID:G65012
 R/Martens, G.J.
 Eur. J. Biochem. 165, 467-472, 1987
 A>Title: Structural organization of the proopiomelanocortin gene in *Xenopus laevis*. 5'-end
 A/Reference number: I51621; MUID:87246627; PMID:3595598
 A/Accession: I51621
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-260 <MAR2>
 A/Cross-references: GB:X05789; NID:G64991; GB:X05941; NID:G64994; GB:X05940; NID:G64992; R/Deen, P.M.T.; Terwel, D.; Bussemakers, M.J.M.; Roubos, E.W.; Martens, G.J.M.
 Eur. J. Biochem. 201, 129-137, 1991
 A>Title: Structural analysis of the entire proopiomelanocortin gene of *Xenopus laevis*.
 A/Reference number: S18009; MUID:92007866; PMID:1915355
 A/Accession: S18009
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-260 <DEE>
 A/Cross-references: EMBL:X59369; NID:G64989; PIDN:CAA42012.1; PID:G64990
 R/Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
 FEBS Lett. 245, 215-218, 1989
 A>Title: Particular processing of pro-opiomelanocortin in *Xenopus laevis* intermediate pituitary cells
 A/Reference number: S03554; MUID:89171310; PMID:2564347
 A/Accession: S03554
 A/Molecule type: protein
 A/Residues: 141-150 <ROU1>
 A/Note: amino end of melanotropin alpha, which is not acetylated in this preparation
 A/Accession: S03555
 A/Molecule type: protein
 A/Residues: 'X', 212-226 <ROU2>
 A/Note: amino end of melanotropin beta
 C/Genetics:
 A/Introns: 43/3
 A/Note: the first intron occurs before the initiator codon
 C/Superfamily: corticotropin-lipotropin
 C/Keywords: glycoprotein; hormone; neuropeptide; opioid peptide; pituitary
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:76-101/Product: melanotropin gamma #status predicted <MTG>
 F:141-179/Product: corticotropin #status predicted <CTN>
 F:141-155/Product: melanotropin alpha #status predicted <MTA>
 F:158-179/Product: CLIP #status predicted <CLP>
 F:182-260/Product: lipotropin beta #status predicted <LTB>
 F:211-227/Product: melanotropin beta #status predicted <MTB>
 F:230-260/Product: beta-endorphin #status predicted <BER>
 F:230-234/Product: Met-enkephalin #status predicted <MEN>
 F:190/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 50; DB 1; Length 260;
 Best Local Similarity 28.3%; Pred. No. 21;
 Matches 13; Conservative 7; Mismatches 8; Indels 18; Gaps 1;
 Mb 154 GRKRPIKVPNGVEESAESFPMELRRELSLELDPEILDDEIE 199
 |||:|
 :|||:|
 :|||:|

RESULT 25
 B38965
 hypothetical protein B - Enterobacter agglomerans insertion sequence IS1222
 C/Species: Enterobacter agglomerans
 C/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C/Accession: B38965; S42922
 R/Steibl, H.D.; Lewecke, F.M.
 Gene 156, 37-42, 1995

Query Match 31.4%; Score 50; DB 2; Length 276;
 Best Local Similarity 43.3%; Pred. No. 22;
 Matches 13; Conservative 3; Mismatches 8; Indels 6; Gaps 1;
 Mb 5 KRORRRDLDEML-----APYIPMDDDF 28
 |||:|
 :|||:|
 :|||:|

Db 85 KRRRRKGLATERPLLRPAAPNLWTWSDDF 114
 |||:|
 :|||:|
 :|||:|

RESULT 26
 DB3741
 hypothetical protein BH0732 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: DB3741
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: DB3741
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-457 <STO>
 A/Cross-references: UNIPROT:Q9KEW7; GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA004
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH0732

Query Match 31.4%; Score 50; DB 2; Length 457;
 Best Local Similarity 40.0%; Pred. No. 38;
 Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 Mb 202 GKKNRKERTGSELHAIREYIPDD 226
 |||:|
 :|||:|
 :|||:|

Db 2 GRKRRRRDLDEMLAPYIPMD 26
 |||:|
 :|||:|
 :|||:|

RESULT 27
 E70610
 hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: E70610
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: E70610
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-561 <COL>
 A/Cross-references: UNIPROT:O05316; GB:Z93777; GB:AL123456; NID:G3261726; PIDN:CAB07817
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: Rv1215c

Query Match 31.4%; Score 50; DB 2; Length 561;
 Best Local Similarity 35.7%; Pred. No. 47;
 Matches 10; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 Mb 2 GRKRRRRDLDEMLAPYIPMD 26
 |||:|
 :|||:|
 :|||:|

A>Title: IS1222: analysis and distribution of a new insertion sequence in *Enterobacter*
 A/Reference number: A38965; MUID:95255664; PMID:7737514
 A/Accession: B38965
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-276 <STB>
 A/Cross-references: UNIPROT:Q46612; GB:X78052; NID:G459246; PIDN:CAA54973.1; PID:G459246
 A/Experimental source: strain Kleeberger, 1983
 C/Genetics:
 A/Mobile element: insertion sequence IS1222

Query Match 31.4%; Score 50; DB 2; Length 276;
 Best Local Similarity 43.3%; Pred. No. 22;
 Matches 13; Conservative 3; Mismatches 8; Indels 6; Gaps 1;
 Mb 5 KRORRRDLDEML-----APYIPMDDDF 28
 |||:|
 :|||:|
 :|||:|

Db 85 KRRRRKGLATERPLLRPAAPNLWTWSDDF 114
 |||:|
 :|||:|
 :|||:|

RESULT 26
 DB3741
 hypothetical protein BH0732 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: DB3741
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: DB3741
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-457 <STO>
 A/Cross-references: UNIPROT:Q9KEW7; GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA004
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH0732

Query Match 31.4%; Score 50; DB 2; Length 457;
 Best Local Similarity 40.0%; Pred. No. 38;
 Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 Mb 202 GKKNRKERTGSELHAIREYIPDD 226
 |||:|
 :|||:|
 :|||:|

Db 2 GRKRRRRDLDEMLAPYIPMD 26
 |||:|
 :|||:|
 :|||:|

RESULT 27
 E70610
 hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: E70610
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: E70610
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-561 <COL>
 A/Cross-references: UNIPROT:O05316; GB:Z93777; GB:AL123456; NID:G3261726; PIDN:CAB07817
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: Rv1215c

Query Match 31.4%; Score 50; DB 2; Length 561;
 Best Local Similarity 35.7%; Pred. No. 47;
 Matches 10; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 Mb 2 GRKRRRRDLDEMLAPYIPMD 26
 |||:|
 :|||:|
 :|||:|

QY 1 YGKRRRRRRDLDLEMLAPVPMDDDF 28
Db 229 WSGRRRTQTQYMEQNEAHLRDDF 256

RESULT 28
T01773
Syntaxin homolog A_IG002P16.16 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01773
R:Miller, N.; Beck, C.; Kramer, J.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002P16.
A:Reference number: Z1421
A:Accession: T01773
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-307 <MIL>
A:Cross-references: EMBL:AF007270; NID:G2191157; PID:G2191179
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 5
A:Introns: 67/2; 159/3; 189/3; 213/3; 249/3; 271/3
A:Note: A_IG002P16.16

Query Match 31.1%; Score 49.5; DB 2; Length 307;
Best Local Similarity 38.7%; Pred. No. 29;
Matches 12; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

QY 1 YGKRRRRRRDLDLEMLAPVPMDDDF 28
Db 180 YLKRLRQKQEDGMDLEMLNLRNRYRPEDDF 210

RESULT 29
F64651
Hypothetical protein HP1054 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64651
R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64651
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-422 <TOM>
A:Cross-references: UNIPROT:O25694; GB:AE000613; GB:AE000511; NID:G2314200; PIDN:AA0810
C:Genetics:
A:Start codon: TTG

Query Match 30.8%; Score 49; DB 2; Length 422;
Best Local Similarity 37.9%; Pred. No. 47;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 YGKRRRRRRDLDLEMLAPVPMDDDF 29
Db 215 FKRKHRLREKIDLSALKDKIAQKEKFQ 243

RESULT 30
G71939
Hypothetical protein jhp0371 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71939

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71939
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-440 <ARN>
A:Cross-references: UNIPROT:Q9ZM52; GB:AE001472; GB:AE001439; NID:G4154897; PIDN:AA0595
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0371

Query Match 30.8%; Score 49; DB 2; Length 440;
Best Local Similarity 37.9%; Pred. No. 50;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 YGKRRRRRRDLDLEMLAPVPMDDDFQ 29
Db 233 FKRKHRLRERDINLSALKDKIAQKEKFQ 261

RESULT 31
B70694
Probable infB - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: B70694
R:Cooper, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70694
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-900 <COL>
A:Cross-references: UNIPROT:P71613; GB:Z81331; GB:AL123456; NID:G3261650; PIDN:CAB03670
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: infB
C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu home
C:Keywords: GTP binding; nucleotide binding; P-loop
F:395-512/Domain: translation elongation factor Tu homology <ETU>
F:405-512/Region: nucleotide-binding motif A (P-loop)
F:509-512/Region: GTP-binding NKXD motif
F:545-547/Region: GTP-binding SAK/L motif
F:411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Asn, Lys, Asp, Ser) #;

Query Match 30.5%; Score 48.5; DB 2; Length 900;
Best Local Similarity 47.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 2 GRKRRRRRRDLDLEMLAPYI 22
Db 277 GRKRRRRRRDLDLEMLAPYI 296

RESULT 32
F87103
Initiation factor IF-2 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87103
R:Cooper, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: F87103

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-924 <STO>

A:Cross-references: UNIPROT:Q9Z519; GB:AL450380; NID:g13093370; PIDN:CAC30507.1; GSPDB:C

C:Genetics:

A:Gene: InfB

C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu homolog

Query Match

Best Local Similarity 30.5%; Score 48.5; DB 2; Length 924;

Matches 10; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 2 GRKKRRQRRDLDEMLAPYI 22

||||:|:|:|:|:|:|:|

DB 301 GRKSKRQKQRYD-SMQAPVW 320

RESULT 33

A70966

hypothetical protein RV2653c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70966

C:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

C:Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

C:Andreasson, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

C:Nature 393, 537-544, 1998

A:Authors: Squires, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70966

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-107 <COL>

A:Cross-references: UNIPROT:P71950; GB:Z80225; GB:AL123456; NID:g3242265; PIDN:CAB02358.

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2653c

C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV2653c

Query Match

Best Local Similarity 30.2%; Score 48; DB 2; Length 107;

Matches 12; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

QY 4 KKRRRRRLD-----LEMLAPYIPMDDD 27

||||:|:|:|:|:|:|:|

DB 39 QRRQRDLRAIRYAEVATSHSIDDD 68

RESULT 34

D71218

hypothetical protein PH0007 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004

C:Accession: D71218

C:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekiri

C:M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

C:DNA Res. 5, 55-76, 1998

A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: D71218

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-232 <XAW>

A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29075.1; PID:g3256392

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0007

C:Superfamily: nucleotidyltransferase

Query Match

Best Local Similarity 30.2%; Score 48; DB 2; Length 232;

Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 YGKRRRRRLDLEMLAPYI 21

||||:|:|:|:|:|:|:|

DB 47 YGSVARGVRRDSDIDIVIPY 67

RESULT 35

D75185

hypothetical protein PAB0004 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 12-Jun-2003

C:Accession: D75185

C:Anonymous, Genoscope

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A:Reference number: A75001

A:Accession: D75185

A:Molecule type: DNA

A:Residues: 1-233 <KAW>

A:Cross-references: GB:A248283; GB:AL096836; NID:g5457433; PIDN:CAB48931.1; PID:g545743

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0004

C:Superfamily: nucleotidyltransferase

Query Match

Best Local Similarity 30.2%; Score 48; DB 2; Length 233;

Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 YGKRRRRRLDLEMLAPYI 21

||||:|:|:|:|:|:|:|

DB 48 YGSVARGVRRDSDIDIVIPY 68

RESULT 36

S35637

high mobility group 1 protein homolog - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004

C:Accession: S35637; I84754

C:Wang, L.; Precht, P.; Balakir, R.; Horton Jr., W.E.

A>Title: Rat and chick cDNA clones encoding HMG-like proteins.

A:Reference number: I50198; MUID:93219134; PMID:8464746

A:Accession: S35636

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 391-476 <WAW>

A:Cross-references: GB:L08814; NID:g203464; PIDN:AAA40927.1; PID:g203465

A:Experimental source: W.E.

C:Genetics:

A:Gene: CIIIDBP

C:Superfamily: HMG box homology

C:Keywords: DNA binding

F396-471/Domain: HMG box homology <HMG1>

Query Match

Best Local Similarity 30.2%; Score 48; DB 2; Length 561;

Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 KKRRRRRLDLEMLAPYIPMDDD 27

||||:|:|:|:|:|:|:|

DB 531 KKRRRRSDSDSEELASTPPSSD 554

RESULT 37

S11218

H1R1 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220

C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein

F;585-781/Domain: ATPase nucleotide-binding domain homology <ATM>

F;213-481/Binding site: carboxylate (Asn) (covalent) #status predicted

F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F;506/Binding site: Asp (Asp) #status predicted

Query Match 30.2%; Score 48; DB 2; Length 1021;

Best Local Similarity 42.3%; Pred. No. 1.6e+02;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 RDLDLEMLAPVPMDDFQL 30

DB 51 RCMELESITRIPQLQDM 70

RESULT 38

A28199

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken

C;Species: Gallus gallus (chicken)

C;Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004

R;Delaveau, T.; Jacq, C.; Perea, J.

R;Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.

J. Biol. Chem. 263, 4347-4354, 1988

A;Title: Ouabain-sensitive (Na⁺ + K⁺)-ATPase activity expressed in mouse L cells by

A;Reference number: A28199; PMID:88153759; PMID:2831227

A;Accession: A28199

A;Status: preliminary

Query Match 30.2%; Score 48; DB 2; Length 840;

Best Local Similarity 45.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 RDLDLEMLAPVPMDDFQL 30

DB 51 RCMELESITRIPQLQDM 70

RESULT 39

A24639

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat

N;Alternate names: UNIPROT:P06685; EMBL:M14511; NID:g203026; PIDN:AAA40775.1; PID:g203030

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758

R;Shull, G.E.; Greeb, J.; Lingrel, J.B.

Biochemistry 25, 8125-8132, 1986

A;Title: Molecular cloning of three distinct forms of the Na⁺, K⁺-ATPase alpha-subunit fr

A;Reference number: A90512; PMID:87128908; PMID:3028470

A;Accession: A24639

A;Molecule type: mRNA

A;Residues: 1-1023 <SHU>

A;Cross-references: UNIPROT:P06685; EMBL:M14511; NID:g203026; PIDN:AAA40775.1; PID:g203030

R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; N

J. Biochem. 102, 43-58, 1987

A;Title: Primary structures of two types of alpha-subunit of rat brain Na⁺, K⁺-ATPase

A;Reference number: S00460; PMID:88032933; PMID:2822882

A;Accession: S00460

A;Molecule type: mRNA

A;Residues: 1-1023 <SHU>

A;Cross-references: UNIPROT:P06685; EMBL:M14511; NID:g203026; PIDN:AAA40775.1; PID:g203030

R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; N

J. Cell Biol. 105, 1855-1865, 1987

A;Title: Three differentially expressed Na⁺, K⁺-ATPase alpha subunit isoforms: structural a

A;Reference number: A92749; PMID:88033255; PMID:2822726

A;Accession: A27180

A;Molecule type: mRNA

A;Residues: 1-1023 <SHU>

A;Cross-references: EMBL:M28647; NID:g205631; PIDN:AAA41671.1; PID:g205632

R;Yagawa, Y.; Kawakami, K.; Nagano, K.

Biochim. Biophys. Acta 1049, 286-292, 1990

A;Title: Cloning and analysis of the 5'-flanking region of rat Na⁺, K⁺-ATPase alpha-1

A;Reference number: S11020; PMID:90344872; PMID:2166579

A;Accession: S11020

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-41 <YAG>

A;Cross-references: EMBL:X52333

R;Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K.J.; Benz Jr., E

Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985

A;Title: Molecular cloning of rat brain Na⁺, K⁺-ATPase alpha-subunit cDNA.

A;Reference number: A25171; PMID:85298352; PMID:2994074

A;Accession: A25171

A;Molecule type: mRNA

A;Residues: 489-533 <SCH>

R;Lyttchen, J.

Biochem. Biophys. Res. Commun. 132, 764-769, 1985

A;Title: The catalytic subunits of the (Na⁺, K⁺)-ATPase alpha and alpha(+) isozymes

A;Reference number: S29877; PMID:86050667; PMID:2998384

A;Accession: S29877

A;Status: preliminary

```

Query March      30.2%; Score 48; DB 2; Length 1023;
Best Local Similarity 36.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GRKRRRRRRDLDEMLAPYIPMD 26
    ||| : : : : : : : : :
19 GDKKKGKGGKDRDMDLKKVSMDD 43

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RESULT 41
Tl3855
suppressor of sable protein homolog - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Tl3855
R:Steinhauer, W.R.; Sterling, J.F.; Graves, J.P.
submitted to the EMBL Data Library, February 1995
A:Description: Comparison of suppressor of sable [su(s)] in two Drosophila species reveal
A:Reference number: Z14224
A:Accession: Tl3855
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1473 <STE>
A:Cross-references: UNIPROT:Q24707; EMBL:U20660; NID:g671708; PIDN:AAA6230
C:Genetics:
A:Cross-references: FlyBase:FBgn0013921
A:Introns: 112/1; 216/3; 702/2; 735/1

Query Match          30.2%; Score 48; DB 2; Length 1473;
Best Local Similarity 40.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      3  RKRRQRRRDLDEMLAPVPM 24
      | : | | | : | | : | |
Db      976  RASAKRRDRDIDNRLFFPM 997

RESULT 42

```

T37242
transforming growth factor beta unc-129 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37242
R:Colavita, A.; Krishna, S.; Zheng, H.; Padgett, R.W.; Culotti, J.G.
Science 281, 706-709, 1998
A:Title: Pioneer axon guidance by UNC-129, a C. elegans TGF-beta.
A:Reference number: Z21640; MUID:98350209; PMID:9685266
A:Accession: T37242
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-407 <COL>
A:Cross-references: UNIPROT:O44371; EMBL:AF029887; NID:g2731819; PIDN:AAC48376.1; PID:g27242
A:Experimental source: strain N2
C:Genetics:
A:Gene: unc-129
A:Map position: IV
A:Function:
A:Description: involved in axonal guidance and guided cell migrations

Query Match 29.9%; Score 47.5; DB 2; Length 407;
Best Local Similarity 37.9%; Pred. No. 73;
Matches 11; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 4 KKRQRRLDLEMLAPY-----IPMDDD 27
:::|||||:::|||||:::|||||
Db 224 EQTKRRDLGNELRELYNYSIPLDND 252

RESULT 43
H90790
hypothetical protein Z1556 [imported] - Escherichia coli (strain O157:H7, substrain EDLS
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85651
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85651
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <STO>
A:Cross-references: UNIPROT:Q8XAK4; GB:AE005174; NID:gl2514427; PIDN:AAG55671.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1556

Query Match 29.9%; Score 47.5; DB 2; Length 462;
Best Local Similarity 37.9%; Pred. No. 84;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 YGRKRRQRRLD-LEMLAPYIPMDDDF 28
|:::|||||:::|||||:::|||||
Db 330 YSRAEQRQRELIDFLNTTGYAPLDQAF 358

RESULT 44
H90790
hypothetical protein ECs1296 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H90790
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90790
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-462 <HAY>
A:Cross-references: UNIPROT:Q8XAK4; GB:BA000007; PIDN:BA034719.1; PID:gl13360756; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1296

Query Match 29.9%; Score 47.5; DB 2; Length 462;
Best Local Similarity 37.9%; Pred. No. 84;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 YGRKRRQRRLD-LEMLAPYIPMDDDF 28
|:::|||||:::|||||:::|||||
Db 330 YSRAEQRQRELIDFLNTTGYAPLDQAF 358

RESULT 45
T20192
hypothetical protein CS3D6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20192
R:Gardner, A.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19235
A:Accession: T20192
A:Status: preliminary; translated from GS/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-563 <WIL>
A:Cross-references: EMBL:Z70270; PIDN:CAA94230.1; GSPDB:GN00022; CESP:C53D6.2
A:Experimental source: clone C53D6
C:Genetics:
A:Gene: CESP:C53D6.2
A:Map position: 4
A:Introns: 42/1; 62/3; 310/3; 385/2; 406/1; 412/1; 464/3; 529/1

Query Match 29.9%; Score 47.5; DB 2; Length 563;
Best Local Similarity 37.9%; Pred. No. 1e+02;
Matches 11; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 4 KKRQRRLDLEMLAPY-----IPMDDD 27
:::|||||:::|||||:::|||||
Db 224 EQTKRRDLGNELRELYNYSIPLDND 252

RESULT 46
S74207
lipoxigenase (EC 1.13.11.12) - cucumber
C:Species: Cucumis sativus (cucumber)
C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S74207; S74137
R:Hoehne, M.; Nellen, A.; Schwennessen, K.; Kindl, H.
Eur. J. Biochem. 241, 6-11, 1996
A:Title: Lipid body lipoxigenase characterized by protein fragmentation, cDNA sequence
A:Reference number: S74137; MUID:97054584; PMID:8898881
A:Accession: S74207
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <HOE>
A:Cross-references: UNIPROT:Q42710; EMBL:X92890; NID:gl296511; PIDN:CAA63483.1
A:Experimental source: tissue cotyledones; clone PCSLBLOX221
A:Accession: S74137

Query Match 29.9%; Score 47.5; DB 2; Length 878;
Best Local Similarity 38.2%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

QY 2 GRKKRRQRRLDLE-MLAP-----YIPMDDDF 28
|:::|||||:::|||||:::|||||
Db 251 GRTGRSRDRDHVESRLSPIMSLDIYVPKDENF 284

RESULT 47

G64139
DNA-directed RNA polymerase (EC 2.7.7.6) omega chain - Haemophilus influenzae (strain Rd
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: G64139
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: G64139
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-88 <TIGR>
A:Cross-references: UNIPROT:P43740; GB:U32848; GB:L42023; NID:G3212240; PIDN:AAC23389.1;
C:Superfamily: DNA-directed RNA polymerase omega chain
C:Keywords: nucleotidyltransferase; RNA biosynthesis; transcription

Query Match 29.6%; Score 47; DB 2; Length 88;

Best Local Similarity 45.0%; Pred. No. 17;

Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 8 QRRRLDLEMLAPYIPMDDD 27

DB 25 RRARQLNQSAFLVPEDND 44

RESULT 48

B82444
hypothetical protein VCA0561 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82444
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <HEI>
A:Cross-references: UNIPROT:Q9KM28; GB:AE004387; GB:AE003853; NID:G9657967; PIDN:AAF9646
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0561
A:Map position: 2

Query Match 29.6%; Score 47; DB 2; Length 124;

Best Local Similarity 37.5%; Pred. No. 25;

Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 7 RRRRLDLEMLAPYIPMDDFQL 30

DB 86 RRRNRDSVPVIFTHAREDDDAEL 109

RESULT 49

A81971
lacto-N-neotetraose biosynthesis glycosyl transferase NNA0525 [imported] - Neisseria men
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: A81971
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: A81971

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-279 <PAR>

A:Cross-references: UNIPROT:P57033; GB:AL162753; GB:AL157959; NID:G7379120; PIDN:CAB88381

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: lgtB; NNA0525

C:Superfamily: lipopolysaccharide biosynthesis-associated protein

Query Match 29.6%; Score 47; DB 2; Length 279;

Best Local Similarity 47.4%; Pred. No. 58;

Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 RKRRRRRLDLEMLAPY 21

DB 260 RKRRRRRLDLEMLAPY 278

RESULT 50

I49585

CD2 antigen protein precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49585

R:Yagita, H.; Okumura, K.; Nakauchi, H.

J. Immunol. 140, 1321-1326, 1988

A:Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule to 1

A:Reference number: I49585; MUID:88140313; PMID:3257775

A:Accession: I49585

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-344 <RES>

A:Cross-references: UNIPROT:P08920; GB:M18934; NID:G192486; PIDN:AAA37397.1; PID:G309158

C:Superfamily: T-cell surface glycoprotein CD2

Query Match 29.6%; Score 47; DB 2; Length 344;

Best Local Similarity 52.9%; Pred. No. 72;

Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RKRRRRRLDLEMLA 19

DB 231 RKRRRRRKDELEIKA 247

Search completed: February 9, 2005, 05:57:35

Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:10:07 ; Search time 43.6842 Seconds
(without alignments)
51.265 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKRRQRRLDLEMLAXYIPMDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	62.1	19	4 US-09-959-873B-8	Sequence 8, Appli
2	95	62.1	34	4 US-09-959-873B-9	Sequence 9, Appli
3	95	62.1	54	4 US-09-438-833-13	Sequence 13, Appli
4	95	62.1	116	4 US-09-438-833-8	Sequence 8, Appli
5	95	62.1	288	4 US-09-438-833-9	Sequence 9, Appli
6	95	62.1	301	4 US-09-438-833-10	Sequence 10, Appli
7	95	62.1	311	4 US-09-438-833-7	Sequence 7, Appli
8	95	62.1	532	4 US-09-949-016-7389	Sequence 7389, Ap
9	95	62.1	613	4 US-09-438-833-6	Sequence 6, Appli
10	95	62.1	652	4 US-09-438-833-5	Sequence 5, Appli
11	95	62.1	756	4 US-09-438-833-11	Sequence 11, Appli
12	95	62.1	805	2 US-08-480-473B-4	Sequence 4, Appli
13	95	62.1	805	3 US-08-915-213-4	Sequence 4, Appli
14	95	62.1	805	3 US-09-235-217-4	Sequence 4, Appli
15	95	62.1	805	5 PCT-US96-10251-4	Sequence 4, Appli
16	95	62.1	810	1 US-08-785-241-7	Sequence 7, Appli
17	95	62.1	813	4 US-09-438-833-12	Sequence 12, Appli
18	95	62.1	826	1 US-08-785-241-6	Sequence 6, Appli
19	95	62.1	826	2 US-08-480-473B-2	Sequence 2, Appli
20	95	62.1	826	3 US-08-915-213-2	Sequence 2, Appli
21	95	62.1	826	3 US-09-148-547-2	Sequence 2, Appli
22	95	62.1	826	3 US-09-235-217-2	Sequence 2, Appli
23	95	62.1	826	3 US-09-380-662-23	Sequence 23, Appli
24	95	62.1	826	4 US-09-438-833-1	Sequence 1, Appli
25	95	62.1	826	4 US-09-702-705-330	Sequence 330, App
26	95	62.1	826	4 US-09-736-457-330	Sequence 330, App
27	95	62.1	826	4 US-09-383-581-2	Sequence 2, Appli

28	95	62.1	826	4 US-09-614-124B-330	Sequence 330, App
29	95	62.1	826	4 US-09-671-325-330	Sequence 330, App
30	95	62.1	826	4 US-09-589-184-330	Sequence 330, App
31	95	62.1	826	4 US-09-658-824-330	Sequence 330, App
32	95	62.1	826	4 US-09-959-873B-18	Sequence 18, Appli
33	95	62.1	826	4 US-09-943-016-6089	Sequence 6089, Ap
34	95	62.1	826	5 PCT-US96-10251-2	Sequence 2, Appli
35	95	62.1	827	4 US-09-919-039-149	Sequence 149, App
36	95	62.1	827	4 US-09-972-784-5	Sequence 5, Appli
37	83	54.2	19	4 US-09-374-454-2	Sequence 2, Appli
38	70.5	46.1	205	3 US-08-785-241-4	Sequence 4, Appli
39	70.5	46.1	870	1 US-08-785-241-4	Sequence 4, Appli
40	70.5	46.1	870	3 US-09-374-454-6	Sequence 6, Appli
41	70.5	46.1	875	1 US-08-785-241-5	Sequence 5, Appli
42	69	45.1	385	1 US-08-450-257-58	Sequence 58, Appli
43	69	45.1	385	1 US-08-450-246-58	Sequence 58, Appli
44	69	45.1	385	1 US-08-450-098-58	Sequence 58, Appli
45	69	45.1	385	1 US-08-451-233-58	Sequence 58, Appli
46	69	45.1	385	1 US-08-450-236-58	Sequence 58, Appli
47	69	45.1	385	3 US-08-235-403-58	Sequence 58, Appli
48	63	41.2	32	2 US-08-706-741B-87	Sequence 87, Appli
49	63	41.2	32	2 US-08-924-695A-87	Sequence 87, Appli
50	60	39.2	28	3 US-09-041-886-50	Sequence 50, Appli
51	60	39.2	28	3 US-09-041-886-56	Sequence 56, Appli
52	60	39.2	134	1 US-08-450-257-38	Sequence 38, Appli
53	60	39.2	134	1 US-08-450-246-38	Sequence 38, Appli
54	60	39.2	134	1 US-08-450-098-38	Sequence 38, Appli
55	60	39.2	134	1 US-08-451-233-38	Sequence 38, Appli
56	60	39.2	134	1 US-08-450-236-38	Sequence 38, Appli
57	60	39.2	134	3 US-08-235-403-38	Sequence 63, Appli
58	60	39.2	143	1 US-08-450-257-63	Sequence 63, Appli
59	60	39.2	143	1 US-08-450-246-63	Sequence 63, Appli
60	60	39.2	143	1 US-08-450-098-63	Sequence 63, Appli
61	60	39.2	143	1 US-08-451-233-63	Sequence 63, Appli
62	60	39.2	143	1 US-08-450-236-63	Sequence 63, Appli
63	60	39.2	143	3 US-08-235-403-63	Sequence 63, Appli
64	58	37.9	11	2 US-08-706-741B-54	Sequence 54, Appli
65	58	37.9	11	2 US-08-924-695A-54	Sequence 54, Appli

ALIGNMENTS

RESULT 1
US-09-959-873B-8
; Sequence 8, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-8

Query Match 62.1%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. NO. 2.2e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2
 US-09-959-873B-9
 ; Sequence 9, Application US/09959873B
 ; Patent No. 6787326
 ; GENERAL INFORMATION:
 ; APPLICANT: Ratcliffe, Peter John
 ; APPLICANT: Maxwell, Patrick Henry
 ; APPLICANT: Pugh, Christopher William
 ; TITLE OF INVENTION: Interaction Between the VHL Tumour
 ; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
 ; TITLE OF INVENTION: Relating Thereto
 ; FILE REFERENCE: 3547.1000-000
 ; CURRENT APPLICATION NUMBER: US/09/959,873B
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: PCT/GB00/01826
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: GB9911047.0
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-09-959-873B-9

Query Match 62.1%; Score 95; DB 4; Length 34;
 Best Local Similarity 94.7%; Pred. No. 4.4e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 3
 US-09-438-833-13
 ; Sequence 13, Application US/09438833
 ; Patent No. 6436654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn
 ; TITLE OF INVENTION: Protein variants
 ; FILE REFERENCE: 1848
 ; CURRENT APPLICATION NUMBER: US/09/438,833
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 54
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
 ; OTHER INFORMATION: 531-584 of human HIF-1 alpha
 US-09-438-833-13

Query Match 62.1%; Score 95; DB 4; Length 54;
 Best Local Similarity 94.7%; Pred. No. 7.7e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 26 DLDLEMLAPYIPMDDDFQL 44

RESULT 4
 US-09-438-833-8
 ; Sequence 8, Application US/09438833
 ; Patent No. 6436654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn
 ; TITLE OF INVENTION: Protein variants
 ; FILE REFERENCE: 1848
 ; CURRENT APPLICATION NUMBER: US/09/438,833
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
 ; OTHER INFORMATION: 526-641 of human HIF-1 alpha
 US-09-438-833-8

Query Match 62.1%; Score 95; DB 4; Length 116;
 Best Local Similarity 94.7%; Pred. No. 1.9e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 5
 US-09-438-833-9
 ; Sequence 9, Application US/09438833
 ; Patent No. 6436654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn
 ; TITLE OF INVENTION: Protein variants
 ; FILE REFERENCE: 1848
 ; CURRENT APPLICATION NUMBER: US/09/438,833
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
 ; OTHER INFORMATION: 526-813 of human HIF-1 alpha
 US-09-438-833-9

Query Match 62.1%; Score 95; DB 4; Length 288;
 Best Local Similarity 94.7%; Pred. No. 5.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 6
 US-09-438-833-10
 ; Sequence 10, Application US/09438833
 ; Patent No. 6436654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn
 ; TITLE OF INVENTION: Protein variants
 ; FILE REFERENCE: 1848
 ; CURRENT APPLICATION NUMBER: US/09/438,833
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 US-09-438-833-10

; SEQ ID NO 10
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10

Query Match 62.1%; Score 95; DB 4; Length 301;
Best Local Similarity 94.7%; Pred. No. 5.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 7
US-09-438-833-7
; Sequence 7, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 331-641 of human HIF-1 alpha
US-09-438-833-7

Query Match 62.1%; Score 95; DB 4; Length 311;
Best Local Similarity 94.7%; Pred. No. 6.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 236 DLDLEMLAPYIPMDDDFQL 244

RESULT 8
US-09-949-016-7389
; Sequence 7389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USBS THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7389
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7389

Query Match 62.1%; Score 95; DB 4; Length 532;
Best Local Similarity 94.7%; Pred. No. 1.2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 262 DLDLEMLAPYIPMDDDFQL 280

RESULT 9
US-09-438-833-6
; Sequence 6, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-438-833-6

Query Match 62.1%; Score 95; DB 4; Length 613;
Best Local Similarity 94.7%; Pred. No. 1.4e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 10
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-652 of human HIF-1 alpha
US-09-438-833-5

Query Match 62.1%; Score 95; DB 4; Length 652;
Best Local Similarity 94.7%; Pred. No. 1.5e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
US-09-438-833-11
; Sequence 11, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants

us-10-032-361-7-rai

Wed Feb 9 06:11:26 2005

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; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438.833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 71-826 of human H1r-1 alpha
US-09-438-833-11

Query Match      62.1%; Score 95; DB 4; Length 756;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      12 DLDLEMLAXYIPMDDDFQL 30
        |||||:|||||
Db      486 DLDLEMLAPYIPMDDDFQL 504

RESULT 12
US-08-480-473B-4
; Sequence 4, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-473B-4

Query Match      62.1%; Score 95; DB 2; Length 805;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      12 DLDLEMLAXYIPMDDDFQL 30
        |||||:|||||
Db      535 DLDLEMLAPYIPMDDDFQL 553

RESULT 13
US-08-480-473B-4
; Sequence 4, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-473B-4

Query Match      62.1%; Score 95; DB 3; Length 805;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      12 DLDLEMLAXYIPMDDDFQL 30
        |||||:|||||
Db      535 DLDLEMLAPYIPMDDDFQL 553

RESULT 14
US-09-235-217-4
; Sequence 4, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
```

; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,473
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/053001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 805 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-235-217-4

Query Match 62.1%; Score 95; DB 3; Length 805;
 Best Local Similarity 94.7%; Pred. No. 1.9e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLLEMLAXYIPMDDDFQL 30
 Db 535 DLLEMLAPYIPMDDDFQL 553

RESULT 15
 PCT-US96-10251-4
 ; Sequence 4, Application PC/TUS9610251
 ; GENERAL INFORMATION:
 ; APPLICANT: The Johns Hopkins University School of Medicine
 ; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/10251
 ; FILING DATE: 06-JUN-1996

; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/053W01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 805 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US96-10251-4

Query Match 62.1%; Score 95; DB 5; Length 805;
 Best Local Similarity 94.7%; Pred. No. 1.9e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLLEMLAXYIPMDDDFQL 30
 Db 535 DLLEMLAPYIPMDDDFQL 553

RESULT 16
 US-08-785-241-7
 ; Sequence 7, Application US/08785241
 ; Patent No. 5695963
 ; GENERAL INFORMATION:
 ; APPLICANT: McKnight, Steven L.
 ; APPLICANT: Russell, David W.
 ; APPLICANT: Tian, Hui
 ; TITLE OF INVENTION: Endothelial PAS Domain Protein
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/785,241
 ; FILING DATE: 17-JAN-1997

; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: UTSD:1229
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 810 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

; US-08-785-241-7
 Query Match 62.1%; Score 95; DB 1; Length 810;
 Best Local Similarity 94.7%; Pred. No. 1.9e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLLEMLAXYIPMDDDFQL 30
 Db 543 DLLEMLAPYIPMDDDFQL 561

RESULT 17
 US-09-438-833-12
 ; Sequence 12, Application US/09438833
 ; Patent No. 6436654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn
 ; TITLE OF INVENTION: Protein variants
 ; FILE REFERENCE: 1848
 ; CURRENT APPLICATION NUMBER: US/09/438,833
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 813
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-813 of human HIF-1 alpha
US-09-438-833-12

Query Match 62.1%; Score 95; DB 4; Length 813;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 18
US-08-785-241-6
; Sequence 6, Application US/08785241
; Patent No. 5695963
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; APPLICANT: Tian, Hui
; TITLE OF INVENTION: Endothelial PAS Domain Protein
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,241
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-241-6

Query Match 62.1%; Score 95; DB 1; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 19
US-08-480-473B-2
; Sequence 2, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-473B-2

Query Match 62.1%; Score 95; DB 2; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 20
US-08-915-213-2
; Sequence 2, Application US/08915213
; Patent No. 6020462
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-213-2

Query Match 62.1%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 21
US-09-148-547-2
; Sequence 2, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
; FILE REFERENCE: 07285/151001
; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-148-547-2

Query Match 62.1%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 22
US-09-235-217-2
; Sequence 2, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-217-2

Query Match 62.1%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 23
US-09-380-662-23
; Sequence 23, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Stephen
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-23

Query Match 62.1%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 24
US-09-438-833-1
; Sequence 1, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 29

US-09-671-325-330
; Sequence 330, Application US/09671325
; Patent No. 6667154

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325

; CURRENT FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 1825

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-671-325-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 30

US-09-589-184-330
; Sequence 330, Application US/09589184
; Patent No. 6686447

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184

; CURRENT FILING DATE: 2000-06-05

; NUMBER OF SEQ ID NOS: 827

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-589-184-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 31

US-09-658-824-330
; Sequence 330, Application US/09658824
; Patent No. 6746846

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824

; CURRENT FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 1788

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-658-824-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 32

US-09-959-873B-18
; Sequence 18, Application US/09959873B
; Patent No. 6787326

GENERAL INFORMATION:

; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods

; FILE REFERENCE: 3547.1000-000

; CURRENT APPLICATION NUMBER: US/09/959,873B

; CURRENT FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: PCT/GB00/01826

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: GB9911047.0

; PRIOR FILING DATE: 1999-05-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-959-873B-18

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

; Sequence 5, Application US/09972784

; Patent No. 6586088

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Bruik, Richard K.

; TITLE OF INVENTION: Prolyl-4-Hydroxylases

; FILE REFERENCE: US/0871

; CURRENT APPLICATION NUMBER: US/09/972,784

; CURRENT FILING DATE: 2001-10-04

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: sequence derived from HIF-a ODD domain.

US-09-972-784-5

Query Match

Best Local Similarity 54.2%; Score 83; DB 4; Length 19;

Mismatches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30

DB 1 DLDLEALAPYIPADDDFQL 19

RESULT 38

US-09-374-454-2

; Sequence 2, Application US/09374454

; Patent No. 6395548

; GENERAL INFORMATION:

; APPLICANT: Lee, Mu-En

; APPLICANT: Maemura, Koji

; APPLICANT: Hsieh, Chung-Ming

; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS

; FILE REFERENCE: 05433/037001

; CURRENT APPLICATION NUMBER: US/09/374,454

; EARLIER FILING DATE: 1999-08-13

; EARLIER APPLICATION NUMBER: US 60/096,515

; EARLIER FILING DATE: 1998-08-14

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-374-454-2

Query Match

Best Local Similarity 46.1%; Score 70.5; DB 3; Length 205;

Mismatches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 12 DLDLEMLAXYIPMD-DDFQL 30

DB 38 ELDLETLAPYIPMDGEDFQL 57

RESULT 39

US-08-785-241-4

; Sequence 4, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

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; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

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; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; APPLICANT: McKnight, Steven L.

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; APPLICANT: Tian, Hui

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; NUMBER OF SEQUENCES: 7

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

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US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

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; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

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;
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; APPLICANT: Tian, Hui
; TITLE OF INVENTION: Endothelial PAS Domain Protein
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,241
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-785-241-5

Query Match 46.1%; Score 70.5; DB 1; Length 875;
Best Local Similarity 75.0%; Pred. No. 0.079; 1; Indels 1; Gaps 1;
Matches 15; Conservative 3; Mismatches 1;

QY 12 DLDLEMLAXYIPMD-DDFOL 30
Db 523 ELDLETLAPYIPMDGEDFOL 542

;
; RESULT 42
; US-08-450-257-58
; Sequence 58, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/450,403

;
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-257-58

Query Match 45.1%; Score 69; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 0.049; 8; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 8;

QY 1 YGRKKRQRRRRLDLEMLAXYIPM 24
Db 2 YGRKKRQRRRRLSQAQLMPSPM 25

;
; RESULT 43
; US-08-450-246-58
; Sequence 58, Application US/08450246
; Patent No. 5670617
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,246
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403

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FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-246-58

Query Match 45.1%; Score 69; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 0.049;
Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 YGKRRRRRDLLEMLXIYPM 24
Db 2 YGKRRRRRPLSQALMPSPM 25

RESULT 44
US-08-450-098-58
Sequence 58, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766

FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-098-58

Query Match 45.1%; Score 69; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 0.049;
Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 YGKRRRRRDLLEMLXIYPM 24
Db 2 YGKRRRRRPLSQALMPSPM 25

RESULT 45
US-08-451-233-58
Sequence 58, Application US/08451233
Patent No. 5747641
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450

Wed Feb 9 06:11:26 2005

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; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-451-233-58

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Query Match 45.1%; Score 69; DB 1; Length 385;
 Best Local Similarity 62.5%; Pred. No. 0.049;
 Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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QY 1 YGKRRRRRLDLEMLAXIYPM 24
    |||||
Db 2 YGKRRRRRLSQALMPSPM 25
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RESULT 46
 US-08-450-236-58
 ; Sequence 58, Application US/08450236
 ; Patent No. 5804604

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; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: B170 CIP 2

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; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-236-58

```

Query Match 45.1%; Score 69; DB 1; Length 385;
 Best Local Similarity 62.5%; Pred. No. 0.049;
 Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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QY 1 YGKRRRRRLDLEMLAXIYPM 24
    |||||
Db 2 YGKRRRRRLSQALMPSPM 25
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RESULT 47
 US-08-235-403-58
 ; Sequence 58, Application US/08235403
 ; Patent No. 6316003

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; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,403
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:

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Wed Feb 9 06:11:26 2005

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; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-50

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Query Match      39.2%; Score 60; DB 3; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.045;
Matches 15; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

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Db      1 GRKKRRQRRRPPGGDLRLAT 23
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Search completed: February 8, 2005, 20:34:02
 Job time : 43.6842 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:15:22 ; Search time 117.895 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKRRQRRLDLEMLAXIPMDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues
Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : Published Applications AA:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	95	62.1	20	14 US-10-101-662A-15	Sequence 15, Appl
3	95	62.1	20	14 US-10-287-670-15	Sequence 15, Appl
4	95	62.1	20	14 US-10-287-670-25	Sequence 25, Appl
5	95	62.1	34	16 US-10-901-583-9	Sequence 9, Appli
6	95	62.1	54	9 US-09-922-958-5	Sequence 5, Appli
7	95	62.1	409	15 US-10-425-833-8	Sequence 8, Appli
8	95	62.1	466	15 US-10-425-833-9	Sequence 9, Appli
9	95	62.1	538	15 US-10-425-833-6	Sequence 6, Appli
10	95	62.1	542	15 US-10-264-049-2606	Sequence 2606, Ap
11	95	62.1	595	15 US-10-425-833-7	Sequence 7, Appli
12	95	62.1	632	15 US-10-425-833-10	Sequence 10, Appl
13	95	62.1	823	14 US-10-205-342-13	Sequence 13, Appl

14	95	62.1	826	9	US-09-922-958-4	Sequence 4, Appli
15	95	62.1	826	9	US-09-833-790-235	Sequence 235, App
16	95	62.1	826	9	US-09-736-457-330	Sequence 330, App
17	95	62.1	826	9	US-09-902-941-330	Sequence 330, App
18	95	62.1	826	9	US-09-843-626-330	Sequence 330, App
19	95	62.1	826	10	US-09-967-388-4	Sequence 4, Appli
20	95	62.1	826	10	US-09-476-300-330	Sequence 330, App
21	95	62.1	826	13	US-10-028-158-23	Sequence 23, Appl
22	95	62.1	826	13	US-10-101-812-10	Sequence 10, Appl
23	95	62.1	826	14	US-10-101-662A-9	Sequence 9, Appli
24	95	62.1	826	14	US-10-101-816-2	Sequence 2, Appli
25	95	62.1	826	14	US-10-017-754-330	Sequence 330, App
26	95	62.1	826	14	US-10-115-987B-14	Sequence 14, Appl
27	95	62.1	826	14	US-10-287-670-9	Sequence 9, Appli
28	95	62.1	826	14	US-10-113-872-330	Sequence 330, App
29	95	62.1	826	14	US-10-423-419-2	Sequence 2, Appli
30	95	62.1	826	15	US-10-283-017-330	Sequence 330, App
31	95	62.1	826	16	US-10-901-583-18	Sequence 18, Appl
32	95	62.1	827	10	US-09-919-039-149	Sequence 149, App
33	95	62.1	827	14	US-10-247-671-137	Sequence 137, App
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35	90	58.8	826	14	US-10-101-816-6	Sequence 6, Appli
36	90	58.8	826	14	US-10-101-816-7	Sequence 7, Appli
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39	81	52.9	297	15	US-10-296-115-933	Sequence 933, App
40	81	52.9	705	14	US-10-154-386-2	Sequence 2, Appli
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43	65	42.5	169	9	US-09-981-286A-7	Sequence 7, Appli
44	63.5	41.5	870	14	US-10-101-816-4	Sequence 4, Appli
45	61.5	40.2	23	13	US-10-024-935-11	Sequence 11, Appl
46	61.5	40.2	23	15	US-10-603-409-11	Sequence 11, Appl
47	61	39.9	22	9	US-09-949-196-8	Sequence 8, Appli
48	61	39.9	22	9	US-09-949-196-32	Sequence 32, Appli
49	61	39.9	23	14	US-10-311-111-34	Sequence 34, Appl
50	61	39.9	107	14	US-10-083-815-71	Sequence 71, Appl
51	60.5	39.5	23	13	US-10-024-935-10	Sequence 10, Appl
52	60.5	39.5	23	15	US-10-603-409-10	Sequence 10, Appl
53	59	38.6	254	16	US-10-437-963-196272	Sequence 196272,
54	58.5	38.2	17	10	US-09-847-946A-141	Sequence 141, App
55	58.5	38.2	17	10	US-09-847-946A-141	Sequence 142, App
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57	58.5	38.2	20	15	US-10-603-409-8	Sequence 8, Appli
58	58.5	38.2	195	9	US-09-949-780-6	Sequence 6, Appli
59	58	37.9	11	9	US-09-779-791A-1	Sequence 1, Appli
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61	58	37.9	11	9	US-09-815-108-9	Sequence 9, Appli
62	58	37.9	11	9	US-09-886-404-13	Sequence 13, Appl
63	58	37.9	11	9	US-09-805-805-8	Sequence 8, Appli
64	58	37.9	11	9	US-09-821-821-24	Sequence 24, Appl
65	58	37.9	11	9	US-09-895-943-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547-1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; PRIORITY FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09

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PRIOR APPLICATION NUMBER: PCT/GB00/01826
 PRIOR FILING DATE: 2000-05-12
 PRIOR APPLICATION NUMBER: GB9911047.0
 PRIOR FILING DATE: 1999-05-12
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Motif
 US-10-901-583-8

Query Match 62.1%; Score 95; DB 16; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.8e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 2
 US-10-101-662A-15
 Sequence 15, Application US/10101662A
 Publication No. US20030022198A1
 GENERAL INFORMATION:
 APPLICANT: Kaelin Jr., William G
 APPLICANT: Livingston, David A
 APPLICANT: Kim, William
 TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
 TITLE OF INVENTION: Therapeutic Methods Thereof
 FILE REFERENCE: 20363-009
 CURRENT APPLICATION NUMBER: US/10/101,662A
 CURRENT FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 60/277,425
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/277,431
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/277,440
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/332,493
 PRIOR FILING DATE: 2001-11-09
 PRIOR APPLICATION NUMBER: 60/345,131
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/342,598
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/345,132
 PRIOR FILING DATE: 2001-12-20
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (9)
 OTHER INFORMATION: Wherein Xaa is hydroxyproline
 US-10-101-662A-15

Query Match 62.1%; Score 95; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 3
 US-10-287-670-15
 Sequence 15, Application US/10287670
 Publication No. US20030150005A1
 GENERAL INFORMATION:
 APPLICANT: Kaelin Jr., et al.
 TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
 TITLE OF INVENTION: Diagnostic and
 TITLE OF INVENTION: Therapeutic Methods Thereof
 FILE REFERENCE: 20363-009CIP1
 CURRENT APPLICATION NUMBER: US/10/287,670
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 10/101,662
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 10/101,812
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 10/101,816
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 60/277,425
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/277,431
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/277,440
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/332,493
 PRIOR FILING DATE: 2001-11-09
 PRIOR APPLICATION NUMBER: 60/345,131
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/342,598
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/345,132
 PRIOR FILING DATE: 2001-12-20
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (9)
 OTHER INFORMATION: Wherein Xaa is hydroxyproline
 US-10-287-670-15

Query Match 62.1%; Score 95; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||:|||||||
 Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 4
 US-10-287-670-25
 Sequence 25, Application US/10287670
 Publication No. US20030150005A1
 GENERAL INFORMATION:
 APPLICANT: Kaelin Jr., et al.
 TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
 TITLE OF INVENTION: Diagnostic and
 TITLE OF INVENTION: Therapeutic Methods Thereof
 FILE REFERENCE: 20363-009CIP1
 CURRENT APPLICATION NUMBER: US/10/287,670
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 10/101,662
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 10/101,812
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 10/101,816

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; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-25

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Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 5
US-10-901-583-9
; Sequence 9, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

Query Match      62.1%; Score 95; DB 16; Length 34;
Best Local Similarity 94.7%; Pred. No. 3.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 6

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US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-5

Query Match      62.1%; Score 95; DB 9; Length 54;
Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
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Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 7
US-10-425-833-8
; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

Query Match      62.1%; Score 95; DB 15; Length 409;
Best Local Similarity 94.7%; Pred. No. 5.4e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
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Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 8
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

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us-10-032-361-7.rapb

Wed Feb 9 06:11:26 2005

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; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 466
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

Query Match          62.1%; Score 95; DB 15; Length 466;
Best Local Similarity 94.7%; Pred. No. 6.3e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 9
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

Query Match          62.1%; Score 95; DB 15; Length 538;
Best Local Similarity 94.7%; Pred. No. 7.3e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 10
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1

Query Match          62.1%; Score 95; DB 15; Length 632;
Best Local Similarity 94.7%; Pred. No. 8.2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 11
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 595
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

Query Match          62.1%; Score 95; DB 15; Length 595;
Best Local Similarity 94.7%; Pred. No. 8.2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 12
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 632
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

Query Match          62.1%; Score 95; DB 15; Length 632;
Best Local Similarity 94.7%; Pred. No. 8.2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
DB 364 DLDLEMLAPYIPMDDDFQL 382

```

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Best Local Similarity 94.7%; Pred. No. 8.8e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 1;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 13
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-048198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Protein: hypoxia-inducible, factor-1 alpha
US-10-205-342-13

Query Match 62.1%; Score 95; DB 14; Length 823;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 14
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020046794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: RUEAS, Jorge
; APPLICANT: PEREIRA, Teresa
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR-1
; FILE REFERENCE: 3743/43008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-4

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574
```

```
RESULT 15
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020086289A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-235

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 16
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 17
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574
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```
US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-330

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 18
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-330

Query Match 62.1%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 19
US-09-967-388-4
; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; TITLE OF INVENTION: WOUND HEALING
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 62.1%; Score 95; DB 10; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 20
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-330

Query Match 62.1%; Score 95; DB 10; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 21
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
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Wed Feb 9 06:11:26 2005

us-10-032-361-7.rapb

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-2

Query Match          62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
   |||||:|||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 25
US-10-017-754-330
; Sequence 330, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andia
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-330

Query Match          62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
   |||||:|||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 26
US-10-115-987B-14
; Sequence 14, Application US/10115987B
; Publication No. US20030148521A1
; GENERAL INFORMATION:
; APPLICANT: Bell, John C.; Stojdl, David F.;
; APPLICANT: Gray, Douglas A.; Sonenberg,
; APPLICANT: Nahum; Lichty, Brian
; TITLE OF INVENTION: Conditionally Replicative and
; TITLE OF INVENTION: Conditionally Active Viruses
; FILE REFERENCE: 42630-0001
; CURRENT APPLICATION NUMBER: US/10/115,987B
; CURRENT FILING DATE: 2002-03-03
; PRIOR APPLICATION NUMBER: US60/281,781
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: EditPad
; SEQ ID NO 14
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Wang et al.
; JOURNAL: Proceedings of the National Academy of Sciences
; VOLUME: 92
; PAGES: 5510-5514
; DATE: 1995
US-10-115-987B-14

Query Match          62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
   |||||:|||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 27
US-10-287-670-9
; Sequence 9, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009C1P1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-9

Query Match          62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
   |||||:|||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 28
US-10-287-670-9
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US-10-113-872-330
; Sequence 330, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-330

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 29
US-10-423-419-2
; Sequence 2, Application US/10423419
; Publication No. US20030176349A1
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/10/423,419
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US/09/383,581
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-419-2

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 30
US-10-283-017-330
; Sequence 330, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Audria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-017-330

Query Match 62.1%; Score 95; DB 15; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 31
US-10-901-583-18
; Sequence 18, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-583-18

Query Match 62.1%; Score 95; DB 16; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 32
US-09-919-039-149
; Sequence 149, Application US/09919039
; Publication No. US20030108871A1

```
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

Query Match 62.1%; Score 95; DB 10; Length 827;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 33
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 137
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CD1
US-10-247-671-137

Query Match 62.1%; Score 95; DB 14; Length 827;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 34
US-10-101-816-5
; Sequence 5, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Mutains of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
```

```
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-5

Query Match 58.8%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.0006;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 35
US-10-101-816-6
; Sequence 6, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Mutains of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 826
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-6

Query Match 58.8%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.0006;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 36

US-10-101-816-7
; Sequence 7, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 826

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein

US-10-101-816-7

Query Match 58.8%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.0006;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 37

US-10-313-643A-5
; Sequence 5, Application US/10313643A
; Publication No. US20030153503A1
; GENERAL INFORMATION:
; APPLICANT: Klaus, Stephen J.
; APPLICANT: Lin, Al Y.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein

US-10-101-816-7

Query Match 58.8%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.0006;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 38

US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
; APPLICANT: Guenzler-Pukall, Volkmar
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
; FILE REFERENCE: FP0600 US
; CURRENT APPLICATION NUMBER: US/10/313,551A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

Query Match 54.2%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.8e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

; APPLICANT: Arend, Michael P.
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: METHODS OF INCREASING ENDOGENOUS ERYTHROPOIETIN (EPO)
; FILE REFERENCE: FP0601 US
; CURRENT APPLICATION NUMBER: US/10/313,643A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-10-313-643A-5

Query Match 54.2%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.8e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

Db 1 DLDLEALAPYIPADDDFQL 19

RESULT 39

US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
; APPLICANT: Guenzler-Pukall, Volkmar
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
; FILE REFERENCE: FP0600 US
; CURRENT APPLICATION NUMBER: US/10/313,551A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-10-313-551A-5

Query Match 54.2%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.8e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

Db 1 DLDLEALAPYIPADDDFQL 19

RESULT 40

US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
; APPLICANT: Guenzler-Pukall, Volkmar
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
; FILE REFERENCE: FP0600 US
; CURRENT APPLICATION NUMBER: US/10/313,551A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-10-313-551A-5

Query Match 54.2%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.8e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

Db 1 DLDLEALAPYIPADDDFQL 19

RESULT 41

US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
; APPLICANT: Guenzler-Pukall, Volkmar
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
; FILE REFERENCE: FP0600 US
; CURRENT APPLICATION NUMBER: US/10/313,551A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-10-313-551A-5

Query Match 54.2%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.8e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||

Db 1 DLDLEALAPYIPADDDFQL 19

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of tat-CCD
US-09-981-286A-7

Query Match 42.5%; Score 65; DB 9; Length 169;
Best Local Similarity 81.2%; Pred. No. 0.34; Mismatches 1; Gaps 0;
Matches 13; Conservative 2; Indels 2; Gaps 0;

QY 1 YGRKKRQRRDLLE 16
|||:|||||:|
DB 2 YGRKKRQRRVWVLE 17
|||:|||||:|

RESULT 44
US-10-101-816-4
; Sequence 4, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-4

Query Match 41.5%; Score 63.5; DB 14; Length 870;
Best Local Similarity 70.0%; Pred. No. 3.4; Mismatches 2; Indels 1; Gaps 1;
Matches 14; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 12 DLDLEMLAXYIPMD-DDFOL 30
:|||||:|||||:|
DB 523 ELDLETAAIYIPMDGGFOL 542
:|||||:|||||:|

RESULT 45
US-10-024-935-11
; Sequence 11, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S

; APPLICANT: Kenneth Walter Bair
; APPLICANT: Yingnan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: 4-31664PI/Prov
; CURRENT APPLICATION NUMBER: US/10/024,935
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-11

Query Match 40.2%; Score 61.5; DB 13; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.11; Mismatches 3; Indels 1; Gaps 1;
Matches 14; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YGRKKRQRRR-DLDLEMLAX 20
|||||:|||||:|
DB 1 YGRKKRQRRRGETDHYLA 21
|||||:|||||:|

RESULT 46
US-10-603-409-11
; Sequence 11, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: Yingnan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; FILE REFERENCE: 4-33243/PI/N1
; CURRENT APPLICATION NUMBER: US/10/603,409
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/024,935
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/EP1 /15006
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-11

Query Match 40.2%; Score 61.5; DB 15; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.11; Mismatches 3; Indels 1; Gaps 1;
Matches 14; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YGRKKRQRRR-DLDLEMLAX 20
|||||:|||||:|
DB 1 YGRKKRQRRRGETDHYLA 21
|||||:|||||:|

RESULT 47
US-09-949-196-8
; Sequence 8, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S

Wed Feb 9 06:11:26 2005

us-10-032-361-7.rapb

```
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-196-8

Query Match          39.9%; Score 61; DB 9; Length 22;
Best Local Similarity 65.0%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAX 20
   |||||
Db 1 YGRKKRRQRRRLDLEMLAX 20
   |||||

RESULT 48
US-09-949-196-32
; Sequence 32, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-196-32

Query Match          39.9%; Score 61; DB 9; Length 22;
Best Local Similarity 65.0%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAX 20
   |||||
Db 1 YGRKKRRQRRRLDLEMLAX 20
   |||||

RESULT 49
US-10-311-111-34
; Sequence 34, Application US/10311111
; Publication No. US20030121065A1
; GENERAL INFORMATION:
; APPLICANT: SHIBA, KIYOTAKA
; TITLE OF INVENTION: MULTIFUNCTIONAL BASE SEQUENCE AND ARTIFICIAL GENE CONTAINING THE
; FILE REFERENCE: 4439-4004
; CURRENT APPLICATION NUMBER: US/10/311,111
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: JP 2000-180997
```

```
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide
US-10-311-111-34

Query Match          39.9%; Score 61; DB 14; Length 23;
Best Local Similarity 60.0%; Pred. No. 0.13;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAX 20
   |||||
Db 1 YGRKKRRQRRRAAEIRROAQ 20
   |||||

RESULT 50
US-10-083-815-71
; Sequence 71, Application US/10083815
; Publication No. US20030026781A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: ENDOGENOUS INHIBITOR OF ATP SYNTHASE, INCLUDING
; TITLE OF INVENTION: TREATMENT FOR DIABETES
; FILE REFERENCE: 660088.435C2
; CURRENT APPLICATION NUMBER: US/10/083,815
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-10-083-815-71

Query Match          39.9%; Score 61; DB 14; Length 107;
Best Local Similarity 65.0%; Pred. No. 0.74;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRLDLEMLAX 20
   |||||
Db 37 YGRKKRRQRRRGWAGSALAV 56
   |||||

Search completed: February 8, 2005, 20:38:03
Job time : 118.895 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 19:40:51 ; Search time 160.526 Seconds
(without alignments)
72.280 Million cell updates/sec

Title: US-10-032-361-7

Perfect score: 153

Sequence: 1 YGRKKRRQRRDLDEMLAXYIPWDDFQL 30

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	30	ABR82380	ABR82380 Hypoxia-i
2	138	90.2	1125	ABP57672	ABP57672 HIF-1 alp
3	138	90.2	1160	ABP57674	ABP57674 HIF-1 alp
4	136.5	89.2	1087	ABP57673	ABP57673 HIF-1 alp
5	136.5	89.2	1122	ABP57675	ABP57675 HIF-1 alp
6	118	77.1	28	AAO23332	AAO23332 Fluoresce
7	95	62.1	19	AAO49912	AAO49912 Human/mur
8	95	62.1	19	AAE30166	AAE30166 Peptide #
9	95	62.1	19	AAE30167	AAE30167 Peptide #
10	95	62.1	19	AAE30144	AAE30144 HIFalpa
11	95	62.1	19	AAE30162	AAE30162 Peptide #
12	95	62.1	19	AAE30172	AAE30172 Human HIF
13	95	62.1	19	AAE30158	AAE30158 HIF-1alp
14	95	62.1	19	ABR82378	ABR82378 Hypoxia-i
15	95	62.1	19	ADP56728	ADP56728 Substrate
16	95	62.1	19	ADP79479	ADP79479 Hypoxia i
17	95	62.1	20	ABP55440	ABP55440 Hypoxia-i
18	95	62.1	20	ADO22337	ADO22337 HIF-1alp
19	95	62.1	29	AAO233501	AAO233501 Murine HI
20	95	62.1	29	AAO23481	AAO23481 Murine HI
21	95	62.1	29	AAO23472	AAO23472 Murine HI
22	95	62.1	29	AAO23499	AAO23499 Murine HI
23	95	62.1	34	AAO49913	AAO49913 Human/mur
24	95	62.1	34	AAE30161	AAE30161 Peptide #
25	95	62.1	34	AAE30151	AAE30151 HIFalpa

26	95	62.1	54	3	AAAY94637	AAAY94637 HIF-1alp
27	95	62.1	54	7	AAO23490	AAO23490 Murine HI
28	95	62.1	54	7	AAO23530	AAO23530 Murine HI
29	95	62.1	54	7	AAO23528	AAO23528 Murine HI
30	95	62.1	54	7	AAO23519	AAO23519 Murine HI
31	95	62.1	54	7	AAO23529	AAO23529 Murine HI
32	95	62.1	54	7	AAO23493	AAO23493 Murine HI
33	95	62.1	116	3	AAAY94632	AAAY94632 HIF-1alp
34	95	62.1	288	3	AAAY94633	AAAY94633 HIF-1alp
35	95	62.1	301	3	AAAY94634	AAAY94634 HIF-1alp
36	95	62.1	311	3	AAAY94631	AAAY94631 HIF-1alp
37	95	62.1	409	8	ADO39389	ADO39389 Chimeric
38	95	62.1	444	4	AAAB68415	AAAB68415 Amino aci
39	95	62.1	466	8	ADO39390	ADO39390 Chimeric
40	95	62.1	538	8	ADO39387	ADO39387 Chimeric
41	95	62.1	542	5	ABP41474	ABP41474 Human ova
42	95	62.1	595	8	ADO39388	ADO39388 Chimeric
43	95	62.1	613	3	AAAY94630	AAAY94630 HIF-1alp
44	95	62.1	613	5	AAU77614	AAU77614 Human hyp
45	95	62.1	632	8	ADO39391	ADO39391 Chimeric
46	95	62.1	652	3	AAAY94629	AAAY94629 HIF-1alp
47	95	62.1	669	3	AAAY84167	AAAY84167 A variant
48	95	62.1	697	3	AAAY84166	AAAY84166 A variant
49	95	62.1	701	3	AAAY84173	AAAY84173 A variant
50	95	62.1	710	3	AAAY84172	AAAY84172 A variant
51	95	62.1	724	3	AAAY84171	AAAY84171 A variant
52	95	62.1	735	6	ABR82375	ABR82375 Hypoxia-i
53	95	62.1	735	8	ADN75066	ADN75066 Human hyp
54	95	62.1	749	3	AAAY84170	AAAY84170 A variant
55	95	62.1	756	3	AAAY94635	AAAY94635 HIF-1alp
56	95	62.1	789	3	AAAY84169	AAAY84169 A variant
57	95	62.1	789	6	ADA18535	ADA18535 Human hyp
58	95	62.1	789	6	ADA18533	ADA18533 Human hyp
59	95	62.1	789	6	ADA18534	ADA18534 Human hyp
60	95	62.1	805	2	AAW05558	AAW05558 Hypoxia i
61	95	62.1	810	5	ABBS7270	ABBS7270 Mouse 1ec
62	95	62.1	813	3	AAAY94636	AAAY94636 HIF-1alp
63	95	62.1	823	6	ABR41951	ABR41951 Rat hypox
64	95	62.1	825	7	ADD44855	ADD44855 Rat prote
65	95	62.1	826	2	AAW06557	AAW06557 Human hyp

ALIGNMENTS

RESULT 1	ABR82380	standard; peptide; 30 AA.
ID	ABR82380	
AC	ABR82380;	
DT	06-NOV-2003	(first entry)
DE	Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.	
KW	HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO; erythropoietin; vascular endothelial growth factor; VEGF; glycolytic; tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.	
OS	Synthetic.	
Key	Location/Qualifiers	
Modified-site	20	/label= Hyp
FT	/note= "hydroxyproline"	
FT		
XX	WO2003057820-A2.	
XX	17-JUL-2003.	
XX	04-OCT-2002; 2002WO-US031699.	
XX	21-DEC-2001; 2001US-00032361.	

```
XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX PI Mcgrath K;
XX DR WPI; 2003-645988/61.
XX XX Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX PS Claim 2; Page 9; 37pp; English.
XX XX The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
CC containing the oxygen-dependent degradation sequence of HIF-1 alpha
XX SQ Sequence 30 AA;

Query Match 100.0%; Score 153; DB 6; Length 30;
Best Local Similarity 96.7%; Pred. No. 5e-14; Indels 0; Gaps 0;
Matches 29; Conservative 1; Mismatches 0;

QY 1 YGRKKRRQRRRLDLEMLAXYIPMDDDFQL 30
Db 1 YGRKKRRQRRRLDLEMLAXYIPMDDDFQL 30

RESULT 2
ABP57672
ID ABP57672 standard; protein; 1125 AA.
XX AC ABP57672;
XX DT 30-APR-2003 (first entry)
XX DE HIF-1 alpha related fusion protein pCH/TAT/3-0 SEQ ID NO:39.
XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200299104-A1.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-00169948.
XX PR 05-JUN-2001; 2001JP-00169949.
XX PA (POKK ) POLA CHEM IND INC.
XX PA (HIRA/) HIRAOKA M.
XX PA (KOND/) KONDOH S.
XX PI Hiraoka M, Kondoh S, Harada H;
XX DR WPI; 2003-148670/14.
XX DR N-PSDB; AB276624.
XX XX New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
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XX PS Example 3; Page 75-78; 144pp; Japanese.
XX CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAXYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
XX SQ fusion protein from the present invention
XX SQ Sequence 1125 AA;

Query Match 90.2%; Score 138; DB 6; Length 1125;
Best Local Similarity 72.5%; Pred. No. 3.2e-10; Indels 10; Gaps 1;
Matches 29; Conservative 1; Mismatches 0;

QY 1 YGRKKRRQRRR-----DLDLEMLAXYIPMDDDFQL 30
Db 11 YGRKKRRQRRRRNPFSTQDTLDLEMLAXYIPMDDDFQL 50

RESULT 3
ABP57674
ID ABP57674 standard; protein; 1160 AA.
XX AC ABP57674;
XX DT 30-APR-2003 (first entry)
XX DE HIF-1 alpha related fusion protein pBAD/3-0 SEQ ID NO:43.
XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200299104-A1.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-00169948.
XX PR 05-JUN-2001; 2001JP-00169949.
XX PA (POKK ) POLA CHEM IND INC.
XX PA (HIRA/) HIRAOKA M.
XX PA (KOND/) KONDOH S.
XX PI Hiraoka M, Kondoh S, Harada H;
XX DR WPI; 2003-148670/14.
XX DR N-PSDB; AB276626.
XX XX New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT
```



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PT and improvement of microbial fermentation.
XX
PS Example 3; Page 95-99; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (1), or encoding a fusion protein containing at least 16
CC residues of (1), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (1) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (1) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (1) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1160 AA;
Query Match 90.2%; Score 138; DB 6; Length 1160;
Best Local Similarity 72.5%; Pred. No. 3.3e-10; Mismatches 0; Indels 10; Gaps 1;
Matches 29; Conservative 1; Mismatches 0; Indels 10; Gaps 1;

QY 1 YGRKKRRQRRR-----DLDEMLAXYIPMDDDFQL 30
| | | | | | | | | | | | | | | | | | | | |
DB 46 YGRKKRRQRRRSNPFSTQDTDLDEMLAPYIPMDDDFQL 85
| | | | | | | | | | | | | | | | | | | | |

RESULT 4
ABP57673
ID ABP57673 standard; protein; 1087 AA.
XX
AC ABP57673;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/557-574 SEQ ID NO:41.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK ) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76625.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic

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PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX
PS Example 3; Page 85-88; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (1), or encoding a fusion protein containing at least 16
CC residues of (1), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (1) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (1) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (1) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1087 AA;
Query Match 89.2%; Score 136.5; DB 6; Length 1087;
Best Local Similarity 90.3%; Pred. No. 5e-10; Mismatches 1; Indels 1; Gaps 1;
Matches 28; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 YGRKKRRQ-RRRDLDEMLAXYIPMDDDFQL 30
| | | | | | | | | | | | | | | | | | | | |
DB 11 YGRKKRRQRRRSLDLEMLAPYIPMDDDFQL 41
| | | | | | | | | | | | | | | | | | | | |

RESULT 5
ABP57675
ID ABP57675 standard; protein; 1122 AA.
XX
AC ABP57675;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/557-574 SEQ ID NO:45.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK ) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76627.
XX

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XX Claim 13; Page 49; 56pp; English.
XX
CC The present invention describes a novel assay for use in identifying
CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC contacting the VHL protein, the HIF-1alpha subunit and the putative
CC modulator under conditions where the former two would normally complex.
CC Modulators of this type are useful in the treatment of cancer and
CC ischaemic conditions such as coronary, cerebral and vascular
CC insufficiency
XX
XX Sequence 19 AA;
SQ

Query Match 62.1%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 12 DLDLEMLAXYIPMDDDFQL 30
DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 8
AAE30166
ID AAE30166 standard; peptide; 19 AA.
XX
AC AAE30166;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #6 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX

Novel isolated polypeptide useful for treating ischemia, wound healing,
auto-, allo-, and xeno-transplantation, systemic high blood pressure,
cancer, or inflammatory disorders.
XX
PS Example 1; Page 247; 256pp; English.
XX

The invention relates to polypeptides having hypoxia inducible factor
(HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
the invention are used for treating conditions such as ischaemia, wound
healing, auto-, allo-, and xeno-transplantation, systemic high blood
pressure, cancer, or inflammatory disorders. They are also used to identify
additional substrates of HIF hydroxylases. Sequences of the invention are
used to design double stranded RNAs for use in RNA interference. They are
used as therapeutic agents and in purification, isolation, or screening
methods involving immuno-precipitation techniques and for detecting
polypeptides in biological samples. The invention is useful in gene
therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;
XX

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 12 DLDLEMLAXYIPMDDDFQL 30
DB 1 DLDLEMLAGYIPMDDDFQL 19

RESULT 9
AAE30167
ID AAE30167 standard; peptide; 19 AA.
XX
AC AAE30167;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #7 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX

Novel isolated polypeptide useful for treating ischemia, wound healing,
auto-, allo-, and xeno-transplantation, systemic high blood pressure,
cancer, or inflammatory disorders.
XX
PS Example 1; Page 247; 256pp; English.
XX

The invention relates to polypeptides having hypoxia inducible factor
(HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
the invention are used for treating conditions such as ischaemia, wound
healing, auto-, allo-, and xeno-transplantation, systemic high blood
pressure, cancer, or inflammatory disorders. They are also used to identify
additional substrates of HIF hydroxylases. Sequences of the invention are
used to design double stranded RNAs for use in RNA interference. They are
used as therapeutic agents and in purification, isolation, or screening
methods involving immuno-precipitation techniques and for detecting
polypeptides in biological samples. The invention is useful in gene
therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;
XX

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 12 DLDLEMLAXYIPMDDDFQL 30
DB 1 DLDLEMLAGYIPMDDDFQL 19

Db	1	DLDEMLAPYIPMDDDFQL 19	
RESULT 10			
AAE30144			
ID	AAE30144	standard; peptide; 19 AA.	
XX	AAE30144;		
AC	24-FEB-2003	(first entry)	
XX	HIFalpha subunit antagonist #1.		
DE	Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;		
XX	wound healing; ischaemia; transplantation; blood pressure; gene therapy;		
KW	antagonist.		
XX	Unidentified.		
OS	Key	Location/Qualifiers	
XX	Modified-site	2	
FT	FT	/label= Hyp	
XX	WO200274981-A2.		
PN	26-SEP-2002.		
XX	21-MAR-2002; 2002WO-GB001381.		
XX	21-MAR-2001; 2001GB-00007123.		
XX	02-AUG-2001; 2001GB-00018952.		
PR	(ISIS-) ISIS INNOVATION LTD.		
XX	Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;		
XX	WPI; 2003-018808/01.		
DR	Novel isolated polypeptide useful for treating ischemia, wound healing,		
XX	auto-, allo-, and xeno-transplantation, systemic high blood pressure,		
PT	cancer, or inflammatory disorders.		
XX	Claim 49; Page 196; 256pp; English.		
PS	The invention relates to polypeptides having hypoxia inducible factor		
XX	(HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and		
CC	3) and nucleic acid molecules encoding such polypeptides. Polypeptides of		
CC	the invention are used for treating conditions such as ischaemia, wound		
CC	healing, auto-, allo-, and xeno-transplantation, systemic high blood		
CC	pressure, cancer, or inflammatory disorders. They are useful in anti-		
CC	sense regulation of the HIF hydroxylase activity and in particular HIF		
CC	prolyl hydroxylase activity within a cell. They are also used to identify		
CC	additional substrates of HIF hydroxylases. Sequences of the invention are		
CC	used to design double stranded RNAs for use in RNA interference. They are		
CC	used as therapeutic agents and in purification, isolation, or screening		
CC	methods involving immuno-precipitation techniques and for detecting		
CC	polypeptides in biological samples. The invention is useful in gene		
CC	therapy. The present sequence is HIFalpha subunit antagonist. This		
CC	sequence is used in the invention		
XX	Sequence 19 AA;		
SQ	Query Match 62.1%; Score 95; DB 6; Length 19;		
	Best Local Similarity 94.7%; Pred. No. 3.6e-06;		
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	12 DLDEMLAXYIPMDDDFQL 30		
	:		
Db	1 DLDEMLAPYIPMDDDFQL 19		
RESULT 11			
AAE30162			
ID	AAE30162	standard; peptide; 19 AA.	
XX	AAE30162;		
AC	24-FEB-2003	(first entry)	
XX	Peptide #2 used to block HIF-1alpha/pVHL interaction.		
DE	Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;		
XX	wound healing; ischaemia; transplantation; blood pressure; gene therapy.		
KW	Unidentified.		
XX	WO200274981-A2.		
PN	26-SEP-2002.		
XX	21-MAR-2002; 2002WO-GB001381.		
XX	21-MAR-2001; 2001GB-00007123.		
XX	02-AUG-2001; 2001GB-00018952.		
PR	(ISIS-) ISIS INNOVATION LTD.		
XX	Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;		
XX	WPI; 2003-018808/01.		
DR	Novel isolated polypeptide useful for treating ischemia, wound healing,		
XX	auto-, allo-, and xeno-transplantation, systemic high blood pressure,		
PT	cancer, or inflammatory disorders.		
XX	Example 1; Page 246; 256pp; English.		
PS	The invention relates to polypeptides having hypoxia inducible factor		
XX	(HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and		
CC	3) and nucleic acid molecules encoding such polypeptides. Polypeptides of		
CC	the invention are used for treating conditions such as ischaemia, wound		
CC	healing, auto-, allo-, and xeno-transplantation, systemic high blood		
CC	pressure, cancer, or inflammatory disorders. They are useful in anti-		
CC	sense regulation of the HIF hydroxylase activity and in particular HIF		
CC	prolyl hydroxylase activity within a cell. They are also used to identify		
CC	additional substrates of HIF hydroxylases. Sequences of the invention are		
CC	used to design double stranded RNAs for use in RNA interference. They are		
CC	used as therapeutic agents and in purification, isolation, or screening		
CC	methods involving immuno-precipitation techniques and for detecting		
CC	polypeptides in biological samples. The invention is useful in gene		
CC	therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL		
CC	interaction. This sequence is used in the invention		
XX	Sequence 19 AA;		
SQ	Query Match 62.1%; Score 95; DB 6; Length 19;		
	Best Local Similarity 94.7%; Pred. No. 3.6e-06;		
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	12 DLDEMLAXYIPMDDDFQL 30		
	:		
Db	1 DLDEMLAPYIPMDDDFQL 19		
RESULT 12			
AAE30172			
ID	AAE30172	standard; peptide; 19 AA.	
XX	AAE30172;		
AC	24-FEB-2003	(first entry)	
XX	Human HIF1-alpha peptide #2.		
DE	Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;		
XX	wound healing; ischaemia; transplantation; blood pressure; gene therapy;		
KW			

KW human; HIF1-alpha.
 XX Homo sapiens.
 OS WO200274981-A2.
 PN 26-SEP-2002.
 XX
 PD 21-MAR-2002; 2002WO-GB001381.
 XX
 PF 21-MAR-2001; 2001GB-00007123.
 XX
 PR 02-AUG-2001; 2001GB-00018952.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
 PI WPI; 2003-018808/01.
 XX
 DR Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.
 XX
 PS Disclosure; Page 252; 256pp; English.
 XX
 CC The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is human HIF1-alpha peptide. This sequence
 CC is used in the invention
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 62.1%; Score 95; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 DB 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 13
 AAE30158
 ID AAE30158 standard; peptide; 19 AA.
 XX
 XX AAE30158;
 AC
 XX 24-FEB-2003 (first entry)
 DT
 XX HIF-1alpha pVHL minimal binding domain.
 DE
 XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
 KW human.
 XX
 OS Homo sapiens.
 OS
 PN WO200274981-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 21-MAR-2002; 2002WO-GB001381.
 XX

XX 21-MAR-2001; 2001GB-00007123.
 PR 02-AUG-2001; 2001GB-00018952.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
 PI WPI; 2003-018808/01.
 XX
 DR Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.
 XX
 PS Example 1; Page 245; 256pp; English.
 XX
 CC The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
 CC This sequence is used in the invention
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 62.1%; Score 95; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 DB 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 14
 ABR82378
 ID ABR82378 standard; peptide; 19 AA.
 XX
 AC ABR82378;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
 KW
 XX HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
 KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
 KW tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9 /label= Hyp
 FT /note= "hydroxyproline"
 XX
 XX WO2003057820-A2.
 XX
 XX 17-JUL-2003.
 XX
 PD 04-OCT-2002; 2002WO-US031699.
 XX
 PF 21-DEC-2001; 2001US-00032361.
 XX
 PR (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Mcgrath K;
 XX DR WPI; 2003-645988/61.
 XX PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 XX PT ubiquitination, and activator of vascular endothelial growth factor
 XX PT transcription useful for treating tissue injuries including wounds,
 XX PT surgical incisions.
 XX PS Claim 2; Page 8; 37pp; English.
 XX CC The invention relates to peptide inhibitors of hypoxia-inducible factor
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor
 CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
 CC for treating tissue injuries including wounds, surgical incisions,
 CC chronic wounds, heart disease and stroke. The present sequence represents
 CC a specific example of HIF-1 alpha peptide inhibitor, containing the
 CC oxygen-dependent degradation sequence of HIF-1 alpha
 XX CC
 XX SQ Sequence 19 AA;
 Query Match 62.1%; Score 95; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 15
 ADP56728
 ID ADP56728 standard; peptide; 19 AA.
 XX AC ADP56728;
 XX DT 09-SEP-2004 (first entry)
 XX DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
 XX KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
 XX KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
 XX KW human; HIF-PH.
 XX OS Homo sapiens.
 XX PN WO2004052285-A2.
 XX PD 24-JUN-2004.
 XX PF 05-DEC-2003; 2003WO-US038690.
 XX PR 06-DEC-2002; 2002US-0431351P.
 XX PR 06-JUN-2003; 2003US-0476331P.
 XX PR 06-JUN-2003; 2003US-0476726P.
 XX PR 04-DEC-2003; 2003US-00729167.
 XX PA (FIBR-) FIBROGEN INC.
 XX PI Fournay PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
 XX PI Seeley TW;
 XX DR WPI; 2004-468689/44.
 XX PT Regulating fat metabolism or fat metabolic process in subjects, by
 XX PT stabilizing human foreskin fibroblasts alpha in subject, thus regulating
 XX PT fat metabolism or fat metabolic process in subject.
 XX PS Example 9; SEQ ID NO 1; 66pp; English.
 XX CC The invention relates to a novel method for regulating fat metabolism or

CC the fat metabolic process in a subject which comprises stabilising human
 CC foreskin fibroblast HIFalpha (hypoxia inducible factor alpha subunit) in
 CC the subject, or administering a compound that inhibits HIF hydroxylase
 CC activity, thus regulating fat metabolism or the fat metabolic process in
 CC the subject. The method of the invention may be useful for regulating fat
 CC metabolism or a fat metabolic process in a subject. The subject is an
 CC animal, preferably a mammal, more preferably human and the method is
 CC performed in a human cell, tissue or organ. The method may be useful for
 CC treating or preventing atherosclerosis, diabetes and obesity in a
 CC subject. The current sequence is that of the substrate peptide of the
 CC invention which is used during a screening assay of human HIF prolyl
 CC hydroxylase (HIF-PH).
 XX SQ Sequence 19 AA;
 Query Match 62.1%; Score 95; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 16
 ADP79479
 ID ADP79479 standard; peptide; 19 AA.
 XX AC ADP79479;
 XX DT 04-NOV-2004 (first entry)
 XX DE Hypoxia inducible factor prolyl hydroxylase substrate peptide.
 XX KW Human; Hypoxia inducible factor prolyl hydroxylase; glucose metabolism;
 KW antidiabetic; anorectic; hypotensive; antilipaeamic; nephrotropic;
 KW neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
 KW enzyme.
 XX OS Homo sapiens.
 XX PN WO2004052284-A2.
 XX PD 24-JUN-2004.
 XX PF 05-DEC-2003; 2003WO-US038689.
 XX PR 06-DEC-2002; 2002US-0431351P.
 XX PR 06-JUN-2003; 2003US-0476331P.
 XX PR 06-JUN-2003; 2003US-0476726P.
 XX PR 04-DEC-2003; 2003US-00729704.
 XX PA (FIBR-) FIBROGEN INC.
 XX PI Guenzler-Pukall V, Klaus SJ, Langsetmo Parobok I, Seeley TW;
 XX DR WPI; 2004-468688/44.
 XX PT Regulating glucose metabolism or glucose metabolic process in subject,
 XX PT involves stabilizing hypoxia inducible factor alpha in subject, or
 XX PT administering to subject compound inhibiting hypoxia inducible factor
 XX PT hydroxylase activity.
 XX PS Example 14; SEQ ID NO 5; 74pp; English.
 XX CC The present sequence is that of a substrate peptide for hypoxia inducible
 CC factor (HIF) prolyl hydroxylase. It was used in an example from the
 CC invention for the identification of compounds useful for HIF alpha
 CC stabilisation. The invention provides methods and compounds for
 CC regulating glucose metabolism by stabilising HIF alpha, especially by
 CC administering a compound that inhibits HIF hydroxylase activity. The
 CC method of stabilising HIF alpha is used in claimed methods for achieving
 CC glucose homeostasis, decreasing blood glucose levels, decreasing glycated

CC haemoglobin levels, altering expression of a glucose regulatory factor,
 CC altering expression of a glycolytic factor, treating or preventing
 CC diabetes, treating or preventing a disorder associated with increased
 CC blood glucose levels (especially diabetes, hyperglycaemia, obesity,
 CC hypertension, hyperlipidaemia, nephropathy, neuropathy, retinopathy,
 CC impaired glucose tolerance, atherosclerosis and vascular disease),
 CC treating or preventing a condition associated with diabetes, decreasing
 CC blood triglyceride levels, reducing insulin resistance, and increasing
 CC glycaemic control in a subject.

XX Sequence 19 AA;

Query Match 62.1%; Score 95; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. NO. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||
 Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 17

ABP55440
 ID ABP55440 standard; peptide; 20 AA.

XX AC ABP55440;

XX DT 05-FEB-2003 (first entry)

XX DE Hypoxia-inducible factor (HIF) 1 alpha peptide.

XX KW Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
 KW ischaemic-related disorder; hypoxia-inducible factor-related disorder;
 KW prolyl hydroxylation; HIF; hypoxic; ischaemic; vasotropic; cardiant;
 KW cerebroprotective; cytostatic; thrombolytic; antidiabetic; nephrotropic;
 KW myocardial infarction; heart disease; stroke; cancer; diabetes;
 KW cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
 KW renal failure; angiogenesis; vascularisation; prolyl hydroxylase.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Modified-site 9 /label= hydroxyproline

XX PN WO200274249-A2.

XX PD 26-SEP-2002.

XX PF 20-MAR-2002; 2002WO-US008886.

XX PR 20-MAR-2001; 2001US-0277425P.

XX PR 20-MAR-2001; 2001US-0277431P.

XX PR 09-NOV-2001; 2001US-0277440P.

XX PR 09-NOV-2001; 2001US-0332334P.

XX PR 09-NOV-2001; 2001US-0332493P.

XX PR 20-DEC-2001; 2001US-0345200P.

XX PR 20-DEC-2001; 2001US-0342598P.

XX PR 20-DEC-2001; 2001US-0345131P.

XX PR 19-MAR-2002; 2002US-00101812.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PI Kaelin WG, Ivan M;

XX DR WPI; 2003-058330/05.

XX PT Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
 PT myocardial infarction, stroke, cancer, thrombosis or renal failure, by
 PT administering a modulator prolyl hydroxylation of hypoxia-inducible
 PT factor (HIF).

XX

PS Disclosure; Page 26; 128pp; English.

XX The present invention describes a method for treating or preventing a
 CC hypoxic-related disorder, ischaemic-related disorder, or hypoxia-
 CC inducible factor (HIF)-related disorder in a subject by administering to
 CC the subject a compound that modulates prolyl hydroxylation of HIF, such
 CC that the hypoxic-, ischaemic-, or HIF-related disorder is treated,
 CC prevented, reversed or stabilised. HIF related sequences can have
 CC vasotropic, cardiant, cerebroprotective, cytostatic, thrombolytic,
 CC antidiabetic, and nephrotropic activities. The method is useful for
 CC treating hypoxia-related disorder, ischaemic-related disorder or HIF-
 CC related disorder. In particular, the hypoxic- or ischaemic-related
 CC disorder is an acute event (e.g. myocardial infarction, heart disease,
 CC stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
 CC event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
 CC especially a chronic event not caused by tissue scarring. The method is
 CC also useful for increasing angiogenesis or vascularisation. The present
 CC sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
 CC peptide which is given in the exemplification of the present invention

XX SQ Sequence 20 AA;

Query Match 62.1%; Score 95; DB 6; Length 20;
 Best Local Similarity 94.7%; Pred. NO. 3.8e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30

|||||:|||||
 Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 18

ADO22337

ID ADO22337 standard; peptide; 20 AA.

XX AC ADO22337;

XX DT 12-AUG-2004 (first entry)

XX DE HIF-1alpha ligand binding site peptide SEQ ID NO:15.

XX KW transgenic; transgenic non-human animal; light-generating fusion protein;
 KW ligand binding site; light-generating polypeptide moiety;
 KW hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
 KW respiratory; cytostatic; vasotropic; virucide; hypoxic condition; cancer;
 KW ischaemia; viral infection; drug screening; drug discovery;
 KW ligand binding site peptide.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004042361-A2.

XX PD 21-MAY-2004.

XX PF 03-NOV-2003; 2003WO-US035154.

XX PR 04-NOV-2002; 2002US-00287670.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PI Kaelin WG, Livingston DM, Kim T;

XX DR WPI; 2004-400725/37.

XX PT New transgenic non-human animal comprising light-generating fusion
 PT protein, useful in diagnosing and treating hypoxic conditions, cancer,
 PT ischemia and viral infections and in drug screening and discovery.

XX PS Disclosure; SEQ ID NO 15; 11pp; English.

XX CC The present invention describes a transgenic non-human animal comprising
 CC a recombinant nucleic acid molecule stably integrated into the genome of

CC the animal, where the molecule encodes a light-generating fusion protein
 CC comprising a ligand binding site and a light-generating polypeptide
 CC moiety. Also described: (1) an isolated cell of the animal; (2) producing
 CC a transgenic non-human animal; (3) identifying a compound capable of
 CC modifying an activity of hypoxia-inducible factor (HIF) 1 alpha; and (4)
 CC detecting hypoxic tissue. The compound has respiratory, cytostatic,
 CC vasotropic and virucide activities. The transgenic non-human animal,
 CC light-generating fusion protein, agents, kits and compositions are useful
 CC in diagnosing and treating hypoxic conditions, cancer, ischaemia and
 CC viral infections and in drug screening and discovery. The present
 CC sequence represents a HIF-1alpha ligand binding site peptide, which is
 CC used in the exemplification of the present invention.

XX SQ Sequence 20 AA;
 Query Match 62.1%; Score 95; DB 8; Length 20;
 Best Local Similarity 94.7%; Pred. No. 3.8e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||
 Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 19
 AAO23501
 ID AAO23501 standard; peptide; 29 AA.

XX AC AAO23501;
 DT 12-FEB-2004 (first entry)
 XX DE Murine HIF-1alpha protein N-TAD region mutant fragment P563A.
 XX KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

XX OS Mus sp.
 XX PN WO2003074560-A2.
 XX PD 12-SEP-2003.
 XX PF 05-MAR-2003; 2003WO-SE000372.
 XX PR 05-MAR-2002; 2002US-0361333P.
 XX PR 27-NOV-2002; 2002US-0429307P.
 XX PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX PI Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.
 XX PS Example 6; Fig 19; 96pp; English.

XX PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX PS Example 6; Fig 19; 96pp; English.
 XX CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic

CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23500-509 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

XX SQ Sequence 29 AA;

Query Match 62.1%; Score 95; DB 7; Length 29;
 Best Local Similarity 94.7%; Pred. No. 5.7e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||
 Db 10 DLDLEMLAYIPMDDDFQL 28

RESULT 20
 AAO23481
 ID AAO23481 standard; peptide; 29 AA.

XX AC AAO23481;
 XX DT 12-FEB-2004 (first entry)
 XX DE Murine HIF-1alpha protein mutant fragment.
 XX KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW mutant.

XX OS Mus sp.

XX PN WO2003074560-A2.

XX PD 12-SEP-2003.

XX PF 05-MAR-2003; 2003WO-SE000372.

XX PR 05-MAR-2002; 2002US-0361333P.

XX PR 27-NOV-2002; 2002US-0429307P.

XX PA (ANGI-) ANGIOGENETICS SWEDEN AB.

XX PI Pereira T, Poellinger L, Hellstroem M;

XX WPI; 2003-712876/67.

XX PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX PS Claim 39; Page 93; 96pp; English.

XX CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing erythropoietin
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a specific example
 CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-


```
CC related conditions
SQ Sequence 29 AA;

Query Match          62.1%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 10 DLDLEMLAPYIPMDDDFQL 28
      |||||:|||||
      |||||:|||||

RESULT 21
AAO23472
ID AAO23472 standard; peptide; 29 AA.
AC AAO23472;
XX
DT 12-FEB-2004 (first entry)
DE Murine HIF-1alpha protein mutant fragment.
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW mutant.
XX
OS Mus sp.
PN WO2003074560-A2.
PD 12-SEP-2003.
PF 05-MAR-2003; 2003WO-SE000372.
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX (ANGI-) ANGIOGENETICS SWEDEN AB.
PA
PI Pereira T, Poellinger L, Hellstroem M;
XX WPI; 2003-712876/67.
DR
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Claim 39; Page 89; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a specific example
CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
CC related conditions
XX
SQ Sequence 29 AA;

Query Match          62.1%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 10 DLDLEMLAPYIPMDDDFQL 28
      |||||:|||||
      |||||:|||||

Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 10 DLDLEMLAPYIPMDDDFQL 28
      |||||:|||||
      |||||:|||||

RESULT 22
AAO23499
ID AAO23499 standard; peptide; 29 AA.
AC AAO23499;
XX
DT 12-FEB-2004 (first entry)
DE Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.
XX
OS Mus sp.
PN WO2003074560-A2.
PD 12-SEP-2003.
PF 05-MAR-2003; 2003WO-SE000372.
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX (ANGI-) ANGIOGENETICS SWEDEN AB.
PA
PI Pereira T, Poellinger L, Hellstroem M;
XX WPI; 2003-712876/67.
DR
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 6; Fig 19; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a N-TAD region of
CC a murine HIF-1 alpha protein
XX
SQ Sequence 29 AA;

Query Match          62.1%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
Db 10 DLDLEMLAPYIPMDDDFQL 28
      |||||:|||||
      |||||:|||||
```


PA (ISIS-) ISIS INNOVATION LTD.
XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
PI WPI; 2003-018808/01.
XX
XX Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
XX Disclosure; Page 239; 256pp; English.
XX
XX The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIF-1alpha subunit antagonist. This
CC sequence is used in the invention
XX
XX Sequence 34 AA;
SQ
Query Match 62.1%; Score 95; DB 6; Length 34;
Best Local Similarity 94.7%; Pred. No. 6.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAXYIPMDDDFOL 30
DB 8 DLDLEMLAXYIPMDDDFOL 26
|||||:|||||
RESULT 26
AA94637
ID AA94637 standard; protein; 54 AA.
XX
XX AA94637;
AC
XX
XX 15-AUG-2000 (first entry)
DT
XX
XX HIF-1alpha variant protein sequence HIF-1alpha/531-584.
DE
XX
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
KW
XX Homo sapiens.
OS
XX WO200029437-A1.
PN
XX 25-MAY-2000.
PD
XX
XX 11-NOV-1999; 99WO-SE002053.
PF
XX
XX 13-NOV-1998; 98SE-00003891.
PR
XX
XX (PHAA) PHARMACIA & UPJOHN AB.
PA
XX
XX Berkenstam A, Poellinger L;
PI
XX
XX WPI; 2000-399715/34.
DR
XX
XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
XX Claim 19; Page 84-85; 87pp; English.
PS

XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aqueora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of HIF-
CC angiogenesis, erythropoiesis an glycolysis
XX
XX Sequence 54 AA;
SQ
Query Match 62.1%; Score 95; DB 3; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAXYIPMDDDFOL 30
DB 26 DLDLEMLAXYIPMDDDFOL 44
|||||:|||||
RESULT 27
AA023490
ID AA023490 standard; peptide; 54 AA.
XX
XX AA023490;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Murine HIF-1alpha protein N-TAD region fragment (residues 531-584).
DE
XX
XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.
XX
XX Mus sp.
OS
XX WO2003074560-A2.
PN
XX
XX 12-SEP-2003.
PD
XX
XX 05-MAR-2003; 2003WO-SE000372.
PF
XX
XX 05-MAR-2002; 2002US-0361333P.
PR
XX
XX 27-NOV-2002; 2002US-0429307P.
PR
XX
XX (ANGI-) ANGIOGENETICS SWEDEN AB.
PA
XX
XX Pereira T, Poellinger L, Hellstrom M;
PI
XX
XX WPI; 2003-712876/67.
DR
XX
XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
XX Example 4; Fig 4; 96pp; English.
PS
XX
XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability

CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis.
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;
 Query Match 62.1%; Score 95; DB 7; Length 54;
 Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 DLDEMLAXYIPMDDDFOL 30
 Db 25 DLDEMLAPYIPMDDDFOL 43
 RESULT 28
 AAO23530
 ID AAO23530 standard; peptide; 54 AA.
 XX
 AC AAO23530;
 XX
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region mutant fragment Q572A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 XX
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX
 PS Example 11; Fig 27; 96pp; English.
 XX
 PT The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 PS Example 11; Fig 27; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein

CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;
 Query Match 62.1%; Score 95; DB 7; Length 54;
 Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 DLDEMLAXYIPMDDDFOL 30
 Db 25 DLDEMLAPYIPMDDDFOL 43
 RESULT 29
 AAO23528
 ID AAO23528 standard; peptide; 54 AA.
 XX
 AC AAO23528;
 XX
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 XX
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX
 PS New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PS angiogenesis, or treating a condition associated with HIF-1alpha
 PS underexpression in a cell, a group of cells, or an organism, e.g.
 PS ischemia or inflammation.
 XX
 PS Example 11; Fig 27; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein

CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;

Query Match 62.1%; Score 95; DB 7; Length 54;
 Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||||
 DB 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 30
 AAO23519
 ID AAO23519 standard; peptide; 54 AA.

XX AAO23519;

AC AAO23519;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein N-TAD region mutant fragment P563A.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

XX Mus sp.

XX WO2003074560-A2.

XX 12-SEP-2003.

XX 05-MAR-2003; 2003WO-SE000372.

XX 05-MAR-2002; 2002US-0361333P.

PR 27-NOV-2002; 2002US-0429307P.

XX (ANGI-) ANGIOGENETICS SWEDEN AB.

XX Pereira T, Poellinger L, Hellstroem M;

DR WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX Example 11; Fig 27; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis.
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenetic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

XX Sequence 54 AA;

Query Match 62.1%; Score 95; DB 7; Length 54;

Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||||
 DB 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 31
 AAO23529
 ID AAO23529 standard; peptide; 54 AA.

XX AAO23529;

AC AAO23529;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

XX Mus sp.

XX WO2003074560-A2.

XX 12-SEP-2003.

XX 05-MAR-2003; 2003WO-SE000372.

XX 05-MAR-2002; 2002US-0361333P.

PR 27-NOV-2002; 2002US-0429307P.

XX (ANGI-) ANGIOGENETICS SWEDEN AB.

XX Pereira T, Poellinger L, Hellstroem M;

DR WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX Example 11; Fig 27; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis.
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenetic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

XX Sequence 54 AA;

Query Match 62.1%; Score 95; DB 7; Length 54;
 Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
 |||||:|||||||
 DB 25 DLDLEMLAPYIPMDDDFQL 43

```

RESULT 32
AAO23493
ID AAO23493 standard; peptide; 54 AA.
XX
AC AAO23493;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment P-A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
XX ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
XX antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
XX N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
XX
PT 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
XX angiogenesis, or treating a condition associated with HIF-1alpha
XX underexpression in a cell, a group of cells, or an organism, e.g.
XX ischemia or inflammation.
XX
PS Example 4; Fig 4; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
XX that has (a) an altered transactivation capacity and improved stability
XX at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
XX pharmaceutical composition are useful for increasing angiogenesis,
XX interfering with a normal response to reoxygenation following hypoxia, or
XX treating a condition associated with HIF-1alpha underexpression in a
XX cell, a group of cells, or an organism, e.g. ischemia, diabetic
XX retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
XX stroke. The proteins and pharmaceutical compositions are also useful for
XX mimicking the hypoxic response or artificially inducing a hypoxic
XX response in a cell, group of cells, or organism, inducing vascular
XX formation or vascular development in a cell or a group of cells,
XX increasing angiogenic activity in a cell, or influencing erythropoietin
XX production, metabolism, or an inflammatory response in a cell, a group of
XX cells, or an organism. Sequences AAO23491-98 represent mutant fragments
XX within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;
Query Match 62.1%; Score 95; DB 7; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 12 DLDLEMLAXYIPMDDDFQL 30
DB 25 DLDLEMLAAYIPMDDDFQL 43
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 33
AAO23493
ID AAY94632 standard; protein; 116 AA.
XX

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AC AAY94632;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
XX that modulate its functional domain and regulate genes involved in
XX angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 76-77; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX multi-step process which includes hypoxia-dependent nuclear import and
XX activation of the transactivation domain. The HIF-1alpha consists of a
XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX nuclear localization sequence located at amino acids 718-584, a
XX transactivator domain (N-TAD) located between amino acids 531 and 584,
XX and a second transactivator domain (C-TAD) located between 813 and 826.
XX The invention relates to isolated variants of HIF-1alpha, such as that
XX represented by the present sequence. The variants are useful for
XX identifying compounds capable of modulating the function of a functional
XX domain of human HIF-1alpha. The method comprises contacting a candidate
XX compound with a cell expressing a HIF-1alpha variant conjugated to a
XX molecular probe. The localization of the probe can be detected in the
XX cell. The Aequorea victoria green fluorescent protein can be used as the
XX molecular probe. The compounds are useful for the regulation of HIF-
XX 1alpha target genes, such as those involved in the regulation of
XX angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 116 AA;
Query Match 62.1%; Score 95; DB 3; Length 116;
Best Local Similarity 94.7%; Pred. No. 2.6e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 12 DLDLEMLAXYIPMDDDFQL 30
DB 31 DLDLEMLAPYIPMDDDFQL 49
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 34
AAO23493
ID AAY94633 standard; protein; 288 AA.
XX
AC AAY94633;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-813.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;

```

KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

XX Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in angiogenesis, erythropoiesis.

PS Claim 13; Page 77-78; 87pp; English.

CC This sequence represents a fragment of the hypoxia-inducible factor (HIF) -alpha amino acid sequence. The mechanism of action of HIF-1alpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-1alpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-1alpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 531 and 584, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-1alpha, such as that represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HIF-1alpha. The method comprises contacting a candidate compound with a cell expressing a HIF-1alpha variant conjugated to a molecular probe. The localization of the probe can be detected in the cell. The Aqueora victoria green fluorescent protein can be used as the molecular probe. The compounds are useful for the regulation of HIF-1alpha target genes, such as those involved in the regulation of angiogenesis, erythropoiesis and glycolysis

XX Sequence 288 AA;

Query Match 62.1%; Score 95; DB 3; Length 288;

Best Local Similarity 94.7%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30

DB 31 DLDLEMLAXYIPMDDDFQL 49

RESULT 35

AA94634

ID AAY94634 standard; protein; 301 AA.

XX AAY94634;

DT 15-AUG-2000 (first entry)

DE HIF-1alpha variant protein sequence HIF-1alpha/526-826.

KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD; regulation; angiogenesis; erythropoiesis; glycolysis; human.

OS Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

XX Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in angiogenesis, erythropoiesis.

PS Claim 13; Page 78-79; 87pp; English.

CC This sequence represents a fragment of the hypoxia-inducible factor (HIF) -alpha amino acid sequence. The mechanism of action of HIF-1alpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-1alpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-1alpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 531 and 584, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-1alpha, such as that represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HIF-1alpha. The method comprises contacting a candidate compound with a cell expressing a HIF-1alpha variant conjugated to a molecular probe. The localization of the probe can be detected in the cell. The Aqueora victoria green fluorescent protein can be used as the molecular probe. The compounds are useful for the regulation of HIF-1alpha target genes, such as those involved in the regulation of angiogenesis, erythropoiesis and glycolysis

XX Sequence 301 AA;

Query Match 62.1%; Score 95; DB 3; Length 301;

Best Local Similarity 94.7%; Pred. No. 7.3e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30

DB 31 DLDLEMLAXYIPMDDDFQL 49

RESULT 36

AA94631

ID AAY94631 standard; protein; 311 AA.

XX AAY94631;

DT 15-AUG-2000 (first entry)

DE HIF-1alpha variant protein sequence HIF-1alpha/331-641.

KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD; regulation; angiogenesis; erythropoiesis; glycolysis; human.

OS Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX New nucleic acid construct for controlling expression of target gene,
PT useful e.g. for treating cancer, is modulated by exogenous
PT pharmaceutical and oxygen partial pressure.
XX Disclosure; Page 57-58; 60pp; French.
XX The specification describes a nucleic acid construct bearing a system for
CC regulating the expression of a gene. The nucleic acid construct comprises
CC at least one sequence encoding a protein that regulates expression of at
CC least one gene of interest. The activity of this protein is modulated by
CC presence/absence of a pharmacological agent and the amount of protein
CC produced depends on the oxygen partial pressure. The constructs are used
CC to treat conditions associated with cellular hypoxia, especially anemia,
CC cancer and ischemia, specifically where the gene of interest encodes
CC erythropoietin (but many other suitable genes are listed, e.g. those
CC encoding single-chain antibodies for immunotherapy of infections or
CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
CC etc.). The present sequence is encoded by the open reading frame of ttrak-
CC hH104. The sequence contains a human hH104 fragment, inserted into the
CC BsiWI site of ttrak. The sequence is used to produce constructs of the
CC invention
XX
SQ Sequence 444 AA;
Query Match 62.1%; Score 95; DB 4; Length 444;
Best Local Similarity 94.7%; Pred. No. 0.00011;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
DB 242 DLDLEMLAPYIPMDDDFQL 260
RESULT 39
ADO39390
ID ADO39390 standard; protein; 466 AA.
XX ADO39390;
AC ADO39390;
XX 15-JUL-2004 (first entry)
DT 15-JUL-2004 (first entry)
XX Chimeric transactivator THV fragment #4.
DE Chimeric transactivator THV fragment #4.
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX Homo sapiens.
OS Homo sapiens.
XX US2004018606-A1.
PN US2004018606-A1.
XX 29-JAN-2004.
PD 29-JAN-2004.
XX 30-APR-2003; 2003US-00425833.
PF 30-APR-2003; 2003US-00425833.
XX 30-APR-2002; 2002US-0376269P.
PR 30-APR-2002; 2002US-0376269P.
XX (BOHL/) BOHL D.
PA (BOHL/) BOHL D.
XX (HEAR/) HEARD M.
PA (HEAR/) HEARD M.
XX Bohl D, Heard M;
PI Bohl D, Heard M;
XX WPI; 2004-122040/12.
DR N-PSDB; ADO39385.
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX Disclosure; Fig 61; 28pp; English.

XX The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC the subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 466 AA;
Query Match 62.1%; Score 95; DB 8; Length 466;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
DB 235 DLDLEMLAPYIPMDDDFQL 253
RESULT 40
ADO39387
ID ADO39387 standard; protein; 538 AA.
XX ADO39387;
AC ADO39387;
XX 15-JUL-2004 (first entry)
DT 15-JUL-2004 (first entry)
XX Chimeric transactivator THV fragment #1.
DE Chimeric transactivator THV fragment #1.
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX Homo sapiens.
OS Homo sapiens.
XX US2004018606-A1.
PN US2004018606-A1.
XX 29-JAN-2004.
PD 29-JAN-2004.
XX 30-APR-2003; 2003US-00425833.
PF 30-APR-2003; 2003US-00425833.
XX 30-APR-2002; 2002US-0376269P.
PR 30-APR-2002; 2002US-0376269P.
XX (BOHL/) BOHL D.
PA (BOHL/) BOHL D.
XX (HEAR/) HEARD M.
PA (HEAR/) HEARD M.
XX Bohl D, Heard M;
PI Bohl D, Heard M;
XX WPI; 2004-122040/12.
DR N-PSDB; ADO39382.
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX Disclosure; Fig 61; 28pp; English.

PS Disclosure; Fig 6F; 28pp; English.

XX The invention describes an isolated polynucleotide (1) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.

XX Sequence 538 AA;

Query Match 62.1%; Score 95; DB 8; Length 538;

Best Local Similarity 94.7%; Pred. No. 0.00014;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFOL 30

Db 364 DLDLEMLAPYIPMDDDFOL 382

RESULT 41

ABP41474

ID ABP41474 standard; protein; 542 AA.

XX AC ABP41474;

XX DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HNOR110, SEQ ID NO:2606.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.

XX Homo sapiens.

XX WO200200677-A1.

XX PD 03-JAN-2002.

XX PF 07-JUN-2001; 2001WO-US018569.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX DR N-PSDB; ABQ54551.

XX

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.

XX Claim 11; SEQ ID NO 2606; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 542 AA;

Query Match 62.1%; Score 95; DB 5; Length 542;

Best Local Similarity 94.7%; Pred. No. 0.00014;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFOL 30

Db 272 DLDLEMLAPYIPMDDDFOL 290

RESULT 42

ADO39388

ID ADO39388 standard; protein; 595 AA.

XX AC ADO39388;

XX DT 15-JUL-2004 (first entry)

XX DE Chimeric transactivator THV fragment #2.

XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.

XX Homo sapiens.

XX US2004018606-A1.

XX PD 29-JAN-2004.

XX PF 30-APR-2003; 2003US-00425833.

XX PR 30-APR-2002; 2002US-0376269P.

XX (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
XX Bohl D, Heard M;
XX
XX WPI; 2004-122040/12.
DR N-P5DB; ADQ39383.
XX
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
XX Disclosure; Fig 6G; 28pp; English.
XX
XX The invention describes an isolated polynucleotide (1) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
XX Sequence 595 AA;
SQ

Query Match 62.1%; Score 95; DB 8; Length 595;
Best Local Similarity 94.7%; Pred. No. 0.00015;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 43
AA94630
XX AA94630 standard; protein; 613 AA.
XX
XX AA94630;
XX
XX 15-AUG-2000 (first entry)
XX
XX HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.
DE
XX
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
KW
XX Homo sapiens.
OS
XX WO200029437-A1.
PN
XX
XX 25-MAY-2000.
PD
XX
XX 11-NOV-1999; 99WO-SE02053.
PF
XX
XX 13-NOV-1998; 98SE-00003891.
PR
XX

PA (PHAA) PHARMACIA & UPJOHN AB.
XX Berkenstam A, Poellinger L;
XX
XX WPI; 2000-399715/34.
XX
XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
XX Claim 13; Page 72-74; 87pp; English.
PS
XX
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis and glycolysis
XX
XX Sequence 613 AA;
SQ

Query Match 62.1%; Score 95; DB 3; Length 613;
Best Local Similarity 94.7%; Pred. No. 0.00016;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXYIPMDDDFQL 30
|||||:|||||
DB 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 44
AAU77614
XX AAU77614 standard; protein; 613 AA.
XX
XX AAU77614;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
DE
XX
XX Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
KW transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
KW circulatory disorder; cancer; hypertension; demyelinating disorder;
KW angiogenesis; sarcoidosis; hepatitis-caused inflammation;
KW chronic ulceration; neovascularisation; arterial hypervascularisation;
KW bullous skin disease; vasculitis; dermatomyositis; polymyositis; mutant;
KW mutein; Y565G.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 177..178
FT /note= "Residues 178-390 of the wild-type HIF-1 have been
FT deleted"
FT
XX WO2000212326-A2.
PN
XX
XX 14-FEB-2002.
PD
XX
XX

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PF 07-AUG-2001; 2001WO-IB001775.
XX
XX
XX 07-AUG-2000; 2000US-0223480P.
XX
XX (ASPE-) ASPERA PHARM AB.
XX
XX Poellinger L, Pereira T, Ruas J;
XX
XX WPI; 2002-257466/30.
XX
XX New polypeptides comprising hypoxia-inducible factor-1 with alterations
XX of the transactivation domain, useful treating ischemic conditions, e.g.
XX brain infarction, heart infarction or circulatory disorder.
XX
XX Example 5; Page; 80pp; English.
XX
XX The invention relates to a polypeptide comprising hypoxia-inducible
XX factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
XX C-TAD). Also included are nucleic acids encoding the altered proteins, a
XX vector comprising the nucleic acid, a host cell transformed with the
XX vector, methods for producing the protein or its functional fragment or
XX an isolated degradation box, a method of screening for an agent that
XX modulates N-TAD function and antagonists, agonists, modulators and HIF-1
XX peptide fragments useful for modulating HIF-1 function or the function of
XX proteins that interact with it. The isolated polypeptides and their
XX fragments with altered residues are useful in methods for treating
XX diseases. The disease is an ischaemic condition, e.g. brain infarction,
XX heart infarction or circulatory disorder. The disease may also be cancer,
XX hypertension, demyelinating disorders, diffuse proliferative
XX glomerulonephritis, toxoplasmosis caused retinochoroiditis, HIV (human
XX immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
XX sarcoma, hepatitis-caused inflammation, hepatitis-caused angiogenesis,
XX chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
XX neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
XX skin disease, vasculitis with angiogenesis, dermatomyositis with
XX angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
XX juvenile osteoarthritis, polyarthritits, aneurysm or atheroma. The present
XX sequence represents HIF-1 mutant delta 178-390. Note: The present
XX sequence is not shown in the specification but was created by the indexer
XX using the information in example 5 and the HIF sequence appearing as
XX AAU77602
XX
XX Sequence 613 AA;
XX
XX Query Match 62.1%; Score 95; DB 5; Length 613;
XX Best Local Similarity 94.7%; Pred. No. 0.00016;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 DLDLEMLAXYIPMDDDFQL 30
XX |||||:|||||
XX Db 343 DLDLEMLAPYIPMDDDFQL 361
XX
XX RESULT 45
XX ADO39391
XX ID ADO39391 standard; protein; 632 AA.
XX
XX AC ADO39391;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX Chimeric transactivator THV fragment #5.
XX
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
XX normoxia; transcription factor degradation; anaemia; AIDS; cancer;
XX inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
XX tetracycline resistance; VP16.
XX
XX Homo sapiens.
XX
XX OS
XX US2004018606-A1.
XX PN
XX 29-JAN-2004.
XX PD
XX
XX 07-AUG-2001; 2001WO-IB001775.
XX
XX 07-AUG-2000; 2000US-0223480P.
XX
XX (ASPE-) ASPERA PHARM AB.
XX
XX Poellinger L, Pereira T, Ruas J;
XX
XX WPI; 2002-257466/30.
XX
XX New polypeptides comprising hypoxia-inducible factor-1 with alterations
XX of the transactivation domain, useful treating ischemic conditions, e.g.
XX brain infarction, heart infarction or circulatory disorder.
XX
XX Example 5; Page; 80pp; English.
XX
XX The invention relates to a polypeptide comprising hypoxia-inducible
XX factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
XX C-TAD). Also included are nucleic acids encoding the altered proteins, a
XX vector comprising the nucleic acid, a host cell transformed with the
XX vector, methods for producing the protein or its functional fragment or
XX an isolated degradation box, a method of screening for an agent that
XX modulates N-TAD function and antagonists, agonists, modulators and HIF-1
XX peptide fragments useful for modulating HIF-1 function or the function of
XX proteins that interact with it. The isolated polypeptides and their
XX fragments with altered residues are useful in methods for treating
XX diseases. The disease is an ischaemic condition, e.g. brain infarction,
XX heart infarction or circulatory disorder. The disease may also be cancer,
XX hypertension, demyelinating disorders, diffuse proliferative
XX glomerulonephritis, toxoplasmosis caused retinochoroiditis, HIV (human
XX immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
XX sarcoma, hepatitis-caused inflammation, hepatitis-caused angiogenesis,
XX chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
XX neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
XX skin disease, vasculitis with angiogenesis, dermatomyositis with
XX angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
XX juvenile osteoarthritis, polyarthritits, aneurysm or atheroma. The present
XX sequence represents HIF-1 mutant delta 178-390. Note: The present
XX sequence is not shown in the specification but was created by the indexer
XX using the information in example 5 and the HIF sequence appearing as
XX AAU77602
XX
XX Sequence 613 AA;
XX
XX Query Match 62.1%; Score 95; DB 5; Length 613;
XX Best Local Similarity 94.7%; Pred. No. 0.00016;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 DLDLEMLAXYIPMDDDFQL 30
XX |||||:|||||
XX Db 343 DLDLEMLAPYIPMDDDFQL 361
XX
XX RESULT 45
XX ADO39391
XX ID ADO39391 standard; protein; 632 AA.
XX
XX AC ADO39391;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX Chimeric transactivator THV fragment #5.
XX
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
XX normoxia; transcription factor degradation; anaemia; AIDS; cancer;
XX inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
XX tetracycline resistance; VP16.
XX
XX Homo sapiens.
XX
XX OS
XX US2004018606-A1.
XX PN
XX 29-JAN-2004.
XX PD
XX
XX 30-APR-2003; 2003US-00425833.
XX
XX 30-APR-2002; 2002US-0376269P.
XX
XX (BOHL/) BOHL D.
XX
XX (HEAR/) HEARD M.
XX
XX Bohl D, Heard M;
XX
XX WPI; 2004-122040/12.
XX
XX N-PSDB; ADO39386.
XX
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
XX of a transcription factor susceptible to degradation under normoxia
XX conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
XX
XX Disclosure; Fig 6J; 28pp; English.
XX
XX The invention describes an isolated polynucleotide (1) which codes for a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions. Also described are: a chimeric transactivator comprising a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions; an isolated polynucleotide which codes for the chimeric
XX transactivator (1); a vector comprising the chimeric transactivator
XX polynucleotide (2); a composition comprising polynucleotide (2) and a
XX polynucleotide which contains a sequence that codes for a target gene and
XX a promoter which is regulated by the chimeric transactivator coded; a
XX method of expressing a target gene in a subject, comprising administering
XX the composition of (4); a method of increasing the number of red blood
XX cells in a subject, comprising administering the composition of (4) to
XX the subject; and a method of increasing the number of blood vessels in
XX subject, comprising administering the composition of (4) to the subject.
XX The methods and compositions of the present invention are useful for
XX treating anaemia associated with AIDS or cancer, anaemia from
XX inflammatory origin and haemoglobinopathies. This is the amino acid
XX sequence of a fragment of a chimeric transactivator comprising regions of
XX the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
XX transcription factor gene and VP16.
XX
XX Sequence 632 AA;
XX
XX Query Match 62.1%; Score 95; DB 8; Length 632;
XX Best Local Similarity 94.7%; Pred. No. 0.00016;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 DLDLEMLAXYIPMDDDFQL 30
XX |||||:|||||
XX Db 235 DLDLEMLAPYIPMDDDFQL 253
XX
XX RESULT 46
XX AAY94629
XX ID AAY94629 standard; protein; 652 AA.
XX
XX AC AAY94629;
XX
XX DT 15-AUG-2000 (first entry)
XX
XX HIF-1alpha variant protein sequence HIF-1alpha/1-652.
XX
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
XX Homo sapiens.
XX
XX OS
XX WO200029437-A1.
XX PN
XX 25-MAY-2000.
XX PD
XX

```

PF 11-NOV-1999; 99WO-SE002053.
 XX
 PR 13-NOV-1998; 98SE-00003891.
 XX
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Berkenstam A, Poellinger L;
 XX WPI; 2000-399715/34.
 DR Human hypoxia-inducible factor alpha variants for identifying compounds
 XX that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 XX
 PS Claim 15; Page 69-70; 87pp; English.
 CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -lalpha amino acid sequence. The mechanism of action of HIF-lalpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transcription domain. The HIF-lalpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-lalpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-lalpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-lalpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-lalpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC lalpha target genes, such as those involved in the regulation of
 CC angiogenesis, erythropoiesis and glycolysis
 XX
 SQ Sequence 652 AA;
 Query Match 62.1%; Score 95; DB 3; Length 652;
 Best Local Similarity 94.7%; Pred. No. 0.00017;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 DB 556 DLDLEMLAPYIPMDDDFQL 574
 |||||:|||||
 RESULT 47
 AAY84167
 ID AAY84167 standard; protein; 669 AA.
 AC AAY84167;
 XX
 DT 03-JUL-2000 (first entry)
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 XX ischemic tissue damage.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 422
 FT /note= "this residue is optionally not Ser, and is
 FT preferably Gly"
 FT Misc-difference 423
 FT /note= "this residue is optionally not Thr, and is
 FT preferably Ala"
 XX
 WO200010578-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US019416.
 XX
 PR 25-AUG-1998; 98US-00148547.
 XX

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX Semenza GL;
 XX WPI; 2000-246493/21.
 DR Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 XX treating hypoxia or ischemia-related tissue damage.
 PT
 PS Claim 1; Page; 96pp; English.
 CC The present sequence represents a variant of hypoxia-inducible factor
 CC (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
 CC protein (see AAY69407). The HIF-lalpha variants are stable under hypoxic
 CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 CC 391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826,
 CC 512-826 or 517-826 of the wild type human HIF-lalpha polypeptide, in
 CC which residues 551 and 552 are not serine and threonine, respectively.
 CC The HIF-lalpha variant polynucleotide sequences are useful for increasing
 CC expression of a hypoxia inducible gene in a cell. They are also useful for
 CC providing constitutive expression of a hypoxia inducible factor in a
 CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-lalpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided
 XX
 SQ Sequence 669 AA;
 Query Match 62.1%; Score 95; DB 3; Length 669;
 Best Local Similarity 94.7%; Pred. No. 0.00017;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFQL 30
 DB 399 DLDLEMLAPYIPMDDDFQL 417
 |||||:|||||
 RESULT 48
 AAY84166
 ID AAY84166 standard; protein; 697 AA.
 AC AAY84166;
 XX
 DT 03-JUL-2000 (first entry)
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 XX ischemic tissue damage.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 422
 FT /note= "this residue is optionally not Ser, and is
 FT preferably Gly"
 FT Misc-difference 423
 FT /note= "this residue is optionally not Thr, and is
 FT preferably Ala"
 XX
 WO200010578-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US019416.
 XX
 PR 25-AUG-1998; 98US-00148547.
 XX

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PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Semenza GL;
PI
XX WPI; 2000-246493/21.
DR
XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX treating hypoxia or ischemia-related tissue damage.
PT
XX Claim 1; Page; 96pp; English.
PS
XX The present sequence represents a variant of hypoxia-inducible factor
XX (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type
XX protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
XX 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX which residues 551 and 552 are not serine and threonine, respectively.
XX The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX expression of a hypoxia inducible gene in a cell. They is also useful for
XX providing constitutive expression of a hypoxia inducible factor in a
XX cell, and for reducing or preventing hypoxia or ischemia related damage.
XX The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX therapy for inducing the level of angiogenesis in tissues of patients at
XX risk of coronary artery disease or ischemic tissue damage. note: this
XX sequence does not appear in the specification; it was created using
XX information provided
XX
XX SQ Sequence 697 AA;

Query Match 62.1%; Score 95; DB 3; Length 697;
Best Local Similarity 94.7%; Pred. No. 0.00018;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDEMLAXYIPMDDDFOL 30
Db 427 DLDEMLAPYIPMDDDFOL 445

RESULT 49
AAY84173
ID AAY84173 standard; protein; 701 AA.
XX
XX AAY84173;
XX
XX 03-JUL-2000 (first entry)
XX
XX A variant of human hypoxia inducible factor-1 alpha protein.
XX
XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
XX hypoxia inducible gene; hypoxia inducible factor; hypoxia;
XX ischemia related damage; angiogenesis; coronary artery disease;
XX ischemic tissue damage.
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 426 /note= "this residue is not Ser, and is preferably Gly"
XX FT Misc-difference 427 /note= "this residue is not Thr, and is preferably Ala"
XX
XX WO200010578-A1.
XX
XX 02-MAR-2000.
XX
XX 25-AUG-1999; 99WO-US019416.
XX
XX 25-AUG-1998; 98US-00148547.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Semenza GL;
XX

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PI Semenza GL;
XX
XX WPI; 2000-246493/21.
DR
XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX treating hypoxia or ischemia-related tissue damage.
PT
XX Claim 1; Page; 96pp; English.
PS
XX The present sequence represents a variant of hypoxia-inducible factor
XX (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type
XX protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
XX 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX which residues 551 and 552 are not serine and threonine, respectively.
XX The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX expression of a hypoxia inducible gene in a cell. They is also useful for
XX providing constitutive expression of a hypoxia inducible factor in a
XX cell, and for reducing or preventing hypoxia or ischemia related damage.
XX The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX therapy for inducing the level of angiogenesis in tissues of patients at
XX risk of coronary artery disease or ischemic tissue damage. note: this
XX sequence does not appear in the specification; it was created using
XX information provided
XX
XX SQ Sequence 701 AA;

Query Match 62.1%; Score 95; DB 3; Length 701;
Best Local Similarity 94.7%; Pred. No. 0.00018;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDEMLAXYIPMDDDFOL 30
Db 431 DLDEMLAPYIPMDDDFOL 449

RESULT 50
AAY84172
ID AAY84172 standard; protein; 710 AA.
XX
XX AAY84172;
XX
XX 03-JUL-2000 (first entry)
XX
XX A variant of human hypoxia inducible factor-1 alpha protein.
XX
XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
XX hypoxia inducible gene; hypoxia inducible factor; hypoxia;
XX ischemia related damage; angiogenesis; coronary artery disease;
XX ischemic tissue damage.
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 435 /note= "this residue is not Ser, and is preferably Gly"
XX FT Misc-difference 436 /note= "this residue is not Thr, and is preferably Ala"
XX
XX WO200010578-A1.
XX
XX 02-MAR-2000.
XX
XX 25-AUG-1999; 99WO-US019416.
XX
XX 25-AUG-1998; 98US-00148547.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Semenza GL;
XX

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DR	WFI; 2000-246493/21.
XX	
PT	Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for treating hypoxia or ischemia-related tissue damage.
PT	
XX	
PS	Claim 1; Page; 96pp; English.
XX	
CC	The present sequence represents a variant of hypoxia-inducible factor (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type protein (see AAY69407). The HIF-alpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 508-826, 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in which residues 551 and 552 are not serine and threonine, respectively.
CC	The HIF-1alpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage.
CC	The variant HIF-1alpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease or ischemic tissue damage. note: this sequence does not appear in the specification; it was created using information provided
CC	
XX	
SQ	Sequence 710 AA;
	Query Match 62.1%; Score 95; DB 3; Length 710;
	Best Local Similarity 94.7%; Pred. No. 0.00019;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	12 DLDLEMLAXYIPMDDDFQL 30 440 DLDLEMLAPYIPMDDDFQL 458
Dd	

Search completed: February 8, 2005, 20:15:10
Job time : 161.526 secs

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OM protein - protein search, using sw model

Run on: February 8, 2005, 19:39:04 ; Search time 148.947 Seconds
(without alignments)
103.140 Million cell updates/sec

Title: US-10-032-361-7

Perfect score: 153

Sequence: 1 YGRKKRRQRRDLLEMLAXYIPMDDFQL 30

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	98	64.1	766	1 HIFA_ONCMY	Q98SW2 oncorhynchu
2	97	63.4	777	2 Q6EH14	Q6eh14 brachydanio
3	96	62.7	774	2 Q6STN7	Q6stn7 ctenopharyn
4	95	62.1	786	2 Q6SL11	Q6sl11 canis famil
5	95	62.1	802	2 Q6FI54	Q6fi54 xenopus lae
6	95	62.1	805	1 HIFA_XENLA	Q918a9 xenopus lae
7	95	62.1	811	1 HIFA_CHICK	Q9yib9 gallus gall
8	95	62.1	819	2 Q7YSE5	Q7yse5 oryctolagus
9	95	62.1	821	2 Q64F54	Q64f54 sparmophilu
10	95	62.1	823	1 HIFA_BOVIN	Q9xta5 bos taurus
11	95	62.1	823	2 Q6IV47	Q6iv47 bos mutus g
12	95	62.1	824	2 Q6H8T3	Q6h8t3 spalax juda
13	95	62.1	825	1 HIFA_RAT	Q35800 rattus norv
14	95	62.1	826	1 HIFA_HUMAN	Q16665 homo sapien
15	95	62.1	836	1 HIFA_MOUSE	Q61221 mus musculu
16	81	52.9	630	2 Q9X54	Q9qx54 mus musculu
17	81	52.9	632	2 Q8WXA1	Q8wxal homo sapien
18	81	52.9	643	2 Q6STN6	Q6stn6 ctenopharyn
19	81	52.9	648	2 Q9HAI2	Q9hai2 homo sapien
20	81	52.9	662	2 Q92215	Q92215 mus musculu
21	81	52.9	667	2 Q9Y2N7	Q9y2n7 homo sapien
22	81	52.9	669	2 Q6K72	Q6k72 homo sapien
23	80	52.3	571	2 Q712E4	Q7tze4 brachydanio
24	80	52.3	626	2 Q6EGR9	Q6egr9 brachydanio
25	78.5	51.3	662	2 Q9JHS2	Q9jhs2 rattus norv
26	76.5	50.0	859	2 Q6GQ12	Q6gq12 xenopus lae
27	74.5	48.7	835	2 Q696W2	Q696w2 ctenopharyn
28	74.5	48.7	862	2 Q6GL61	Q6gl61 xenopus tro
29	74.5	48.7	862	2 Q6GP97	Q6gp97 xenopus lae
30	74.5	48.7	873	2 Q8QGM4	Q8qgm4 fundulus he
31	74	48.4	632	2 Q96K34	Q96k34 homo sapien

ALIGNMENTS

RESULT 1

ID	HIFA	ONCMY	STANDARD	PRT	766 AA.
AC	Q98SW2				
DT	10-OCT-2003	(Rel. 42, Created)			
DT	10-OCT-2003	(Rel. 42, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).				
GN	Name=HIF1A;				
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
OX	NCBI_TaxID=8022;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;				
RA	Soitamo A.J., Babergh C.M.I., Gassmann M., Sistonen L., Nikinmaa M.;				
RT	"Characterization of a hypoxia-inducible factor (HIF-1 alpha) from rainbow trout: accumulation of protein occurs at normal venous oxygen tension.";				
RL	J. Biol. Chem. 276:19699-19705(2001).				
CC	- FUNCTION: Functions as a master transcriptional regulator of the adaptive response to hypoxia. Binds to core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response element (HRE) of target gene promoters. Activation requires recruitment of transcriptional coactivators (By similarity).				
CC	- SUBUNIT: Efficient DNA binding requires heterodimerization of an alpha and a beta/ARNT subunit (By similarity).				
CC	- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear translocation in response to hypoxia (By similarity).				
CC	- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.				
CC	- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.				
CC	- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.				

Q6ryd1 sus scrofa
Q6ryd0 ovis aries
Q9w7c6 gallus gall
Q99814 homo sapien
Q9xc44 bos taurus
Q9pbc3 coturnix co
P97481 mus musculu
Q9jhs1 rattus norv
Q6peu2 mus musculu
Q71939 human immun
Q71945 human immun
Q69628 human immun
Q71264 human immun
Q8ad2c human immun
P88699 human immun
Q6ek47 human immun
Q72493 human immun
Q6eg25 human immun
Q8ad18 human immun
Q902t6 human immun
Q8e7z3 human immun
Q7rje0 human immun
Q8ggi5 fundulus he
Q8aik6 human immun
Q8aik7 human immun
Q69627 human immun
Q69632 human immun
Q69635 human immun
Q69637 human immun
Q69638 human immun
Q69639 human immun
Q69641 human immun
Q6gxz1 human immun
Q70498 human immun

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CC -----
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CC -----
DR EMBL; AF304864; AAK30364.1; -.
DR HSP; Q16665; IH2K.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR Activator; DNA-binding; Nuclear protein; Repeat;
KW Transcription regulation.
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 82 159 PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 368 373 Poly-Glu.
SQ SEQUENCE 766 AA; 85049 MW; FC25A4984104DA5B CRC64;

Query Match 64.1%; Score 98; DB 1; Length 766;
Best Local Similarity 82.6%; Pred. No. 7.8e-05;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRDLLEMLAXYIPMDDDFQL 30
Db 547 QMEDLLEMLAPYIPMDDDFQL 569

RESULT 2
Q6EH14 PRELIMINARY; PRT; 777 AA.
AC Q6EH14
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia inducible factor 1 alpha.
GN Name=hlfa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY326951; AAQ91619.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindfIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

Query Match 62.7%; Score 96; DB 2; Length 774;
Best Local Similarity 82.6%; Pred. No. 0.00015;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRDLLEMLAXYIPMDDDFQL 30
Db 543 QAIEDLLEMLAPYIPMDDDFQL 565

RESULT 4
Q6SL11 PRELIMINARY; PRT; 786 AA.
AC Q6SL11

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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 777 AA; 85897 MW; A9APE2D2732C7A33 CRC64;

Query Match 63.4%; Score 97; DB 2; Length 777;
Best Local Similarity 82.6%; Pred. No. 0.00011;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRDLLEMLAXYIPMDDDFQL 30
Db 545 QPMEDLLEMLAPYIPMDDDFQL 567

RESULT 3
Q6STN7 PRELIMINARY; PRT; 774 AA.
AC Q6STN7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1alpha.
GN Name=hlf-1alpha;
OS Ctenopharyngodon idella (Gloss carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OC NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY450269; AAR95697.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindfIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 774 AA; 85741 MW; 15BD082F90C611C6 CRC64;

Query Match 62.7%; Score 96; DB 2; Length 774;
Best Local Similarity 82.6%; Pred. No. 0.00015;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 QRRDLLEMLAXYIPMDDDFQL 30
Db 543 QAIEDLLEMLAPYIPMDDDFQL 565

RESULT 4
Q6SL11 PRELIMINARY; PRT; 786 AA.
AC Q6SL11

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DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha subunit (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Spee B. Penning L.C., Rothuizen J.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY455802; AAR19225.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAC; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 FT NON_TER 1
 FT NON_TER 786
 SQ SEQUENCE 786 AA; 88015 MW; C37A27C25C343CDC CRC64;

 Query Match 62.1%; Score 95; DB 2; Length 786;
 Best Local Similarity 94.7%; Pred. No. 0.00021;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 12 DLDLEMLAXIYIPDDDFQL 30
 |||||:|||||
 DB 536 DLDLEMLAPYIPDDDFQL 554

 RESULT 5
 Q6P154 PRELIMINARY; PRT; 802 AA.
 AC Q6P154;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DE Hif1a-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uslan T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC043769; AAH43769.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001321; HypoxindFIA.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAC; 2.
 DR PRINTS; PR01080; HYPOXIAFIA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00888; HLH; 1.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 802 AA; 90177 MW; 30A571277A9A5B1F CRC64;

 Query Match 62.1%; Score 95; DB 2; Length 802;
 Best Local Similarity 94.7%; Pred. No. 0.00022;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 12 DLDLEMLAXIYIPDDDFQL 30
 |||||:|||||
 DB 550 DLDLEMLAPYIPDDDFQL 568

 RESULT 6
 HIFA_XENLA STANDARD; PRT; 805 AA.
 ID HIFA_XENLA
 AC Q918A9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=HIF1A;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kietzmann T.;
 RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
 RT 1 alpha homologue.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 CC adaptive response to hypoxia. Binds to core DNA sequence 5'-

```

CC [AG]CTGTG-3' within the hypoxia response element (HRE) of target
CC gene promoters. Activation requires recruitment of transcriptional
CC coactivators (By similarity).
CC
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC
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CC
CC EMBL; AJ277829; CAB96628.1; -.
CC HSP; Q16665; IH2K.
CC InterPro; IPR001092; HLH_basic.
CC InterPro; IPR001321; Hypoxindf1A.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC Pfam; PF00785; PAC; 1.
CC PRINTS; PR01080; HYPOXIAFLA.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00091; PAS; 2.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00091; PAS; 2.
CC PROSITE; PS00888; HLH; 1.
CC PROSITE; PS0112; PAS; 2.
CC Activator; DNA-binding; Nuclear protein; Repeat;
KW Transcription regulation.
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 85 157 PAS 1.
FT DOMAIN 229 300 PAS 2.
FT DOMAIN 303 346 PAC.
FT SEQUENCE 805 AA; 90964 MW; BABFA0BD6544FF3B CRC64;

Query Match 62.1%; Score 95; DB 1; Length 805;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDEMLAXYIPMDDDFQL 30
Db 552 DLDEMLAXYIPMDDDFQL 570
|||||:|||||
552 DLDEMLAXYIPMDDDFQL 570

RESULT 7
HIFA_CHICK STANDARD; PRT; 811 AA.
ID HIFA_CHICK
AC Q9YIB9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Takahashi T.;
RT "Molecular cloning and expression of an avian cDNA for hypoxia-
RT inducible factor-1 alpha in embryonic ventricular myocytes."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the

```

```

CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC [AG]CTGTG-3' within the hypoxia response element (HRE) of target
CC gene promoters. Activation requires recruitment of transcriptional
CC coactivators (By similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB013746; BAA34234.2; -.
CC HSP; Q16665; IH2K.
CC InterPro; IPR001092; HLH_basic.
CC InterPro; IPR001321; Hypoxindf1A.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC Pfam; PF00785; PAC; 1.
CC Pfam; PF00785; PAC; 1.
CC PRINTS; PR01080; HYPOXIAFLA.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00091; PAS; 2.
CC PROSITE; PS00888; HLH; 1.
CC PROSITE; PS0112; PAS; 2.
CC Activator; DNA-binding; Nuclear protein; Repeat;
KW Transcription regulation.
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 80 157 PAS 1.
FT DOMAIN 228 298 PAS 2.
FT DOMAIN 302 345 PAC.
FT DOMAIN 401 587 ODD.
FT DOMAIN 529 573 NTAD.
FT DOMAIN 576 785 ID.
FT DOMAIN 703 706 Nuclear localization signal (Potential).
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DOMAIN 771 811 CTAD.
FT DOMAIN 583 588 Poly-Ser.
FT SEQUENCE 811 AA; 90542 MW; DL4CD9FC98F064CB CRC64;

Query Match 62.1%; Score 95; DB 1; Length 811;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDEMLAXYIPMDDDFQL 30
Db 554 DLDEMLAXYIPMDDDFQL 572
|||||:|||||
554 DLDEMLAXYIPMDDDFQL 572

RESULT 8
QYISE5 PRELIMINARY; PRT; 819 AA.
ID QYISE5
AC QYISE5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia inducible factor 1 alpha subunit.
DE Oryctolagus cuniculus (Rabbit).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
(1)
RN SEQUENCE FROM N.A.
RP Clausen I.; Kietz S.; Fischer B.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC EMBL; AY273790; AAP43517.1; -.
DR HSSP; Q16665; 1H2K.
DR GO; GO:0004871; P: signal transducer activity; IEA.
DR GO; GO:0006355; P: regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 819 AA; 91284 MW; E11B4PBF7B4F6C7C CRC64;

Query Match 62.1%; Score 95; DB 2; Length 819;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXIYPMDDDFQL 30
Db 556 DLDLEMLAXIYPMDDDFQL 574

RESULT 9
Q64F54
ID Q64F54 PRELIMINARY; PRT; 821 AA.
AC Q64F54;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RA Morin P. Jr.; Storey K.B.;
RT "Cloning and expression of HIF-1 from the hibernating ground squirrel,
RT Sperophilus tridecemlineatus."
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY113478; RAU14021.1; -.
SQ SEQUENCE 821 AA; 92028 MW; 4C96BD0355CCCE06 CRC64;

Query Match 62.1%; Score 95; DB 2; Length 821;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDLEMLAXIYPMDDDFQL 30
Db 556 DLDLEMLAXIYPMDDDFQL 574

RESULT 10
HIFA BOVIN
ID HIFA BOVIN STANDARD; PRT; 823 AA.
AC Q9XTA5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
(1)
RN SEQUENCE FROM N.A.
RP TISSUE=Artery;
RC MEDLINE=9255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA Hara S.; Kobayashi C.; Imura N.;
RT "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF) -
RT 1alpha and -2alpha of bovine arterial endothelial cells."
RL Biochim. Biophys. Acta 1445:237-243(1999).
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-564.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC nitrosylated in vivo (By similarity).
CC -1- PTM: Acetylation of Lys-532 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
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CC -----
CC EMBL; AB018398; BAA78675.1; -.
CC HSSP; Q16665; 1L8C.
CC InterPro; IPR001092; HLH_basic.
CC InterPro; IPR001321; HypoxindF1A.

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DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00333; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
KW Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT DOMAIN 718 721
FT DNA BIND 17 30
FT Helix-loop-helix motif.
FT DOMAIN 31 71
FT Helix-loop-helix motif.
FT DOMAIN 85 158
FT PAS 1.
FT DOMAIN 228 298
FT PAS 2.
FT DOMAIN 302 345
FT PAS.
FT DOMAIN 401 600
FT ODD.
FT DOMAIN 531 575
FT NTAD.
FT DOMAIN 576 782
FT ID.
FT DOMAIN 715 718
FT CTAD.
FT MOD_RES 90 90
FT S-nitrosocysteine (Potential).
FT MOD_RES 139 139
FT S-nitrosocysteine (Potential).
FT MOD_RES 173 173
FT S-nitrosocysteine (Potential).
FT MOD_RES 194 194
FT S-nitrosocysteine (Potential).
FT MOD_RES 210 210
FT S-nitrosocysteine (Potential).
FT MOD_RES 219 219
FT S-nitrosocysteine (Potential).
FT MOD_RES 224 224
FT S-nitrosocysteine (Potential).
FT MOD_RES 255 255
FT S-nitrosocysteine (Potential).
FT MOD_RES 334 334
FT S-nitrosocysteine (Potential).
FT MOD_RES 337 337
FT S-nitrosocysteine (Potential).
FT MOD_RES 359 359
FT S-nitrosocysteine (Potential).
FT MOD_RES 402 402
FT Hydroxyproline (By similarity).
FT MOD_RES 520 520
FT S-nitrosocysteine (Potential).
FT MOD_RES 532 532
FT N6-acetyllysine (By similarity).
FT MOD_RES 564 564
FT Hydroxyproline (By similarity).
FT MOD_RES 755 755
FT S-nitrosocysteine (Potential).
FT MOD_RES 777 777
FT S-nitrosocysteine (Potential).
FT MOD_RES 797 797
FT S-nitrosocysteine (Potential).
FT MOD_RES 800 800
FT 3-hydroxyasparagine (By similarity).
SQ SEQUENCE 823 AA; 92127 MW; 12674B467A61B1A1 CRC64;

Query Match 62.1%; Score 95; DB 1; Length 823;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDEMLAXYIPMDDDFQL 30
DB 556 DLDEMLAPYIPMDDDFQL 574
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RESULT 11
Q6IV47 PRELIMINARY; PRT; 823 AA.
AC Q6IV47; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1a.
GN Name-HIF-1a.
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=30521;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolt K.S., Qadar Pasha M.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

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DR EMBL; AY621118; AAT39520.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 823 AA; 92128 MW; A6E388E4FEA15705 CRC64;

Query Match 62.1%; Score 95; DB 2; Length 823;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 DLDEMLAXYIPMDDDFQL 30
DB 556 DLDEMLAPYIPMDDDFQL 574
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|||||

RESULT 12
Q6H8T3 PRELIMINARY; PRT; 824 AA.
AC Q6H8T3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor 1 alpha.
GN Name-hif-1a.
OS Scalax judaei (Blind subterranean mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Spalax.
OC NCBI_TaxID=134510;
RN [1]
RP SEQUENCE FROM N.A.
RA Shams I., Aviati A., Nevo E.;
RL "Hypoxic stress tolerance of the subterranean mole rat: Expression of erythropoietin and hypoxia-inducible factor-1a.";
RL Nucleic Acids Res. 0:0-0(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=15210955; DOI=10.1073/pnas.0403540101;
RA Shams I., Aviati A., Eviatar N.;
RT "Hypoxic stress tolerance of the blind subterranean mole rat: expression of erythropoietin and hypoxia-inducible factor 1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9698-9703(2004).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ715791; CAG29396.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.

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DR PRINTS; PR01080; HYPOXIAIF1A.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 DR SEQUENCE 824 AA; 92161 MW; 33A1DDC3593CBFFP CRC64;
 Query Match 62.1%; Score 95; DB 2; Length 824;
 Best Local Similarity 94.7%; Pred. NO. 0.00022;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPNDDDFQL 30
 DB 556 DLDLEMLAXYIPNDDDFQL 574
 RESULT 13
 ID_HIFA_RAT STANDARD; PRT; 825 AA.
 AC Q35800; Q9WTU9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=Hif1a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Hepatocytes;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivenous expression of the mRNA of the three hypoxia-inducible
 factor a-subunits Hif-1a, Hif2a and Hif3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=21417706; PubMed=11526200;
 RA Zou A.-F., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
 RT "Oxygen-dependent expression of hypoxia-inducible factor-lalpha in
 renal medullary cells of rats.";
 RL Physiol. Genomics 6:159-168(2001).
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 CC adaptive response to hypoxia. Under hypoxic conditions activates
 CC the transcription of over 40 genes, including, erythropoietin,
 CC glucose transporters, glycolytic enzymes, vascular endothelial
 CC growth factor, and other genes whose protein products increase
 CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
 CC Plays an essential role in embryonic vascularization, tumor
 CC angiogenesis and pathophysiology of ischemic disease. Binds to
 CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
 CC element (HRE) of target gene promoters. Activation requires
 CC recruitment of transcriptional coactivators such as CREBBP and
 CC EP300. Activity is enhanced by interaction with both, NCOA1 or
 CC NCOA2. Interaction with redox regulatory protein APEX seems to
 CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
 CC similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
 CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 CC translocation in response to hypoxia (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
 CC seen in the renal medulla than in the cortex. Expressed also in
 CC the perivenous zone of the liver.
 CC -!- DOMAIN: Contains two independent C-terminal transactivation
 CC domains, NTAD and CTAD, which function synergistically. Their
 CC transcriptional activity is repressed by an intervening inhibitory
 CC domain (ID) (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
 CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
 CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
 CC The hydroxylated prolines promote interaction with VHL, initiating
 CC rapid ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
 CC abrogating interaction with CREBBP and EP300 and preventing
 CC transcriptional activation (By similarity).
 CC -!- PTM: S-nitrosylated. All free thiol groups are subjected to S-
 CC nitrosylation in vitro, however not all thiol groups seem to be
 CC nitrosylated in vivo (By similarity).
 CC -!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
 CC and stimulates subsequent proteasomal degradation (By similarity).
 CC -!- PTM: Phosphorylation is required for DNA binding (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; Y09507; CAA70701.1; -.
 CC EMBL; AF057308; AAD24413.1; -.
 CC HSSP; Q16665; IL8C.
 CC TRANSFAC; T05461; -.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001321; HypoxindfIA.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR01080; HYPOXIAIF1A.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS50888; HLH; 1.
 CC PROSITE; PS50112; PAS; 2.
 CC Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
 CC Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
 CC DOMAIN 718 721 Nuclear localization signal (Potential).
 CC DNA BIND 17 30 Basic motif.
 CC DOMAIN 31 71 Helix-loop-helix motif.
 CC DOMAIN 85 158 PAS 1.
 CC DOMAIN 228 298 PAS 2.
 CC DOMAIN 302 345 PAC.
 CC DOMAIN 401 602 ODD.
 CC DOMAIN 530 574 NTAD.
 CC DOMAIN 575 784 ID.
 CC DOMAIN 717 720 Nuclear localization signal (Potential).
 CC DOMAIN 785 825 CTAD.
 CC MOD_RES 90 139 S-nitrosocysteine (Potential).
 CC MOD_RES 139 199 S-nitrosocysteine (Potential).
 CC MOD_RES 173 173 S-nitrosocysteine (Potential).
 CC MOD_RES 194 194 S-nitrosocysteine (Potential).
 CC MOD_RES 210 210 S-nitrosocysteine (Potential).
 CC MOD_RES 219 219 S-nitrosocysteine (Potential).
 CC MOD_RES 224 224 S-nitrosocysteine (Potential).
 CC MOD_RES 255 255 S-nitrosocysteine (Potential).
 CC MOD_RES 334 334 S-nitrosocysteine (Potential).
 CC MOD_RES 337 337 S-nitrosocysteine (Potential).
 CC MOD_RES 385 385 S-nitrosocysteine (Potential).
 CC MOD_RES 402 402 Hydroxyproline (By similarity).
 CC MOD_RES 519 519 S-nitrosocysteine (Potential).
 CC MOD_RES 531 531 N6-acetyllysine (By similarity).

FT	MOD_RES	563	563	Hydroxyproline (By similarity).	RT	"Hypoxia-inducible factor-1 alpha variant isolated from human liver tissue."	
FT	MOD_RES	779	779	S-nitrosocysteine (Potential).	RT	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
FT	MOD_RES	799	799	S-nitrosocysteine (Potential).	RN	[7]	
FT	MOD_RES	802	802	3-hydroxyasparagine (By similarity).	RP	SEQUENCE FROM N.A. (ISOFORM 1).	
FT	CONFLICT	12	74	K -> NR (in Ref. 2).	RC	TISSUE=Choriocarcinoma, and Placenta;	
FT	CONFLICT	12	74	D -> G (in Ref. 2).	RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
FT	CONFLICT	74	96	P -> L (in Ref. 2).	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
FT	CONFLICT	96	96	D -> N (in Ref. 2).	RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,	
FT	CONFLICT	329	329	D -> N (in Ref. 2).	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
FT	CONFLICT	613	619	ATAATAT -> TATA (in Ref. 2).	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
FT	CONFLICT	708	708	R -> K (in Ref. 2).	RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,	
SQ	SEQUENCE	825 AA; 92319 MW; C4109A57F38667E9 CRC64;			RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,	
Query Match					RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
Best Local Similarity					RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
QY					RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
Db					RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
12 DLDLEMLAXYIPMDDDFQL 30					RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
555 DLDLEMLAXYIPMDDDFQL 573					RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RESULT 14					RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
HIFA HUMAN					RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
ID	HIFA HUMAN	STANDARD;	PRT;	826 AA.	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
AC	Q16565; Q96PT9; Q9UPB1;				RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
DT	01-NOV-1997 (Rel. 35, Created)				RT	"Generation and initial analysis of more than 15,000 full-length human	
DT	01-NOV-1997 (Rel. 35, Last sequence update)				RL	and mouse cDNA sequences."	
DT	25-OCT-2004 (Rel. 45, Last annotation update)				RP	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
DE	Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT				RN	[8]	
DE	interacting protein) (Member of PAS protein 1) (MOP1).				RP	TRANSACTIVATION DOMAINS NTAD AND CTAD.	
GN	Name=HIF1A;				RX	MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;	
OS	Homo sapiens (Human).				RA	Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				RT	"Transactivation and inhibitory domains of hypoxia-inducible factor	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				RT	1 alpha. Modulation of transcriptional activity by oxygen tension.";	
OX	NCBI_TaxID=9606;				RL	J. Biol. Chem. 272:19253-19260(1997).	
RN	[1]				RN	[9]	
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.				RP	SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.	
RX	MEDLINE=95396340; PubMed=7539918;				RX	MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;	
RA	Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;				RA	Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,	
RA	"Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS				RA	Poellinger L.;	
RA	heterodimer regulated by cellular O2 tension.";				RT	"Signal transduction in hypoxic cells: inducible nuclear translocation	
RA	Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).				RT	and recruitment of the CBP/p300 coactivator by the hypoxia-inducible	
RL	[2]				RL	factor-1alpha.";	
RP	SEQUENCE FROM N.A.				RL	EMBO J. 17:6573-6586(1998).	
RP	TISSUE=Hepatoma;				RN	[10]	
RX	MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;				RP	OXYGEN-DEPENDENT DEGRADATION DOMAIN.	
RA	Hogness J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,				RX	MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;	
RA	Pray-Grant M., Perdew G.H., Bradfield C.A.;				RA	Huang L.E., Gu J., Schau M., Bunn H.F.;	
RA	"Characterization of a subset of the basic-helix-loop-helix-PAS				RT	"Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-	
RA	superfamily that interacts with components of the dioxin signaling				RT	dependent degradation domain via the ubiquitin-proteasome pathway.";	
RA	pathway.";				RL	Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).	
RL	J. Biol. Chem. 272:8591-8593(1997).				RN	[11]	
RP	SEQUENCE FROM N.A. (ISOFORM 1).				RP	TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND	
RN	[3]				RP	MUTAGENESIS OF CVS-800.	
RX	MEDLINE=99008035; PubMed=9782081; DOI=10.1006/geno.1998.5416;				RX	MEDLINE=9213869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;	
RA	Iyer N.V., Leung S.W., Semenza G.L.;				RA	Emm M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,	
RA	"The human hypoxia-inducible factor 1alpha gene: HIF1A structure and				RA	Poellinger L., Fujii-Kuriyama Y.;	
RA	evolutionary conservation.";				RT	"Molecular mechanisms of transcription activation by HIF and HIF1alpha	
RL	Genomics 52:159-165(1998).				RT	in response to hypoxia: their stabilization and redox signal-induced	
RN	[4]				RL	interaction with CBP/p300.";	
RP	SEQUENCE FROM N.A.				RL	EMBO J. 18:1905-1914(1999).	
RP	Rupert J.L., Hochachka P.W.;				RN	[12]	
RA	"HIF1A sequence in the Quechua, a high altitude population.";				RP	INTERACTION WITH NCOA1, NCOA2 AND APEX.	
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				RX	MEDLINE=20063199; PubMed=10594042;	
RL	[5]				RA	Carrero P., Okamoto K., Coumalleau P., O'Brien S., Tanaka H.,	
RN	SEQUENCE FROM N.A. (ISOFORM 1).				RA	Poellinger L.;	
RC	TISSUE=Glial tumor;				RT	"Redox-regulated recruitment of the transcriptional coactivators CREB-	
RC	Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;				RT	binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";	
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				RL	Mol. Cell. Biol. 20:402-415(2000).	
RN	[6]				RN	[13]	
RP	SEQUENCE FROM N.A. (ISOFORM 2).				RP	MUTAGENESIS OF SER-551 AND THR-552.	
RC	TISSUE=Liver;				RX	MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;	
RA	Tanaka S., Sugimachi K.;				RA	Sutter C.H., Laughner E., Semenza G.L.;	
					RT	"Hypoxia-inducible factor 1alpha protein expression is controlled by	

RT oxygen-regulated ubiquitination that is disrupted by deletions and
 RL missense mutations.";
 RA Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
 RN [14]
 RP UBIQUITINATION.
 RX MEDLINE=2121430; PubMed=11292861; DOI=10.1126/science.1059796;
 RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
 RA Gaskell S.J., von Kriesheim A., Hebestreit H.F., Mukherji M.,
 RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
 RT "Targeting of HIF-1alpha to the von Hippel-Lindau ubiquitylation
 RT complex by O2-regulated prolyl hydroxylation.";
 RL Science 292:468-472(2001).
 RN [15]
 RP S-NITROSYLATION.
 RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
 RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
 RT "HIF-1 alpha protein as a target for S-nitrosation.";
 RL FEBS Lett. 535:106-112(2003).
 RN [16]
 RP ACETYLATION OF LYS-532.
 RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
 RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
 RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
 RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
 RT acetylation.";
 RL Cell 111:709-720(2002).
 RN [17]
 RP HYDROXYLATION OF ASN-803.
 RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
 RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
 RA Bruck R.K.;
 RT "FIR-1 is an asparaginyl hydroxylase enzyme that regulates the
 RT transcriptional activity of hypoxia-inducible factor.";
 RL Genes Dev. 16:1466-1471(2002).
 RN [18]
 RP HYDROXYLATION OF PRO-402 AND PRO-564.
 RX MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
 RA Bruck R.K., McKnight S.L.;
 RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
 RL Science 294:1337-1340(2001).
 RN [19]
 RP REVIEW.
 RX MEDLINE=20407247; PubMed=10950862;
 RA Semenza G.L.;
 RT "HIF-1 and human disease: one highly involved factor.";
 RL Genes Dev. 14:1983-1991(2000).
 RN [20]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=20539371; PubMed=11089639;
 RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
 RA Michiels C.;
 RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
 RT 1) and its consensus DNA sequence.";
 RL J. Biomol. Struct. Dyn. 18:169-179(2000).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
 RP HIF1AN.
 RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
 RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.F.,
 RA Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
 RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
 RT mechanism of oxidative modification of HIF-1 alpha.";
 RL J. Biol. Chem. 278:1802-1806(2003).
 RN [22]
 RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
 RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
 RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
 RA Wagner G., Eck M.J.;
 RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
 RT factor-1 alpha.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
 RN [23]
 RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.

RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
 RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
 RA Wright P.E.;
 RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular
 RT
 Query Match 62.1%; Score 95; DB 1; Length 826;
 Best Local Similarity 94.7%; Pred. No. 0.00022;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 DLDLEMLAXYIPMDDDFOL 30
 |||||:|||||
 DB 556 DLDLEMLAPYIPMDDDFOL 574
 |||||:|||||
 RESULT 15
 ID_HIFA_MOUSE STANDARD; PRT: 836 AA
 AC Q61221; Q08741; Q08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
 AC Q8R385; Q9CYA8;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
 DE interacting protein).
 GN Name=Hif1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Hepatocytes;
 RX MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
 RA Li H., Ko H.P., Whitlock J.P. Jr.;
 RT "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
 RT Roles of Arnt and Hif1alpha.";
 RL J. Biol. Chem. 271:21262-21267(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129/SvJ;
 RX MEDLINE=98034461; PubMed=9368100;
 RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
 RA Bradfield C.A.;
 RT "Molecular characterization of the murine Hif-1 alpha locus.";
 RL Gene Expr. 6:287-299(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=129/SvJ;
 RX MEDLINE=97354184; PubMed=9210478;
 RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
 RA Gassmann M.;
 RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
 RT organization, expression and characterization of an alternative first
 RT exon and 5' flanking sequence.";
 RL Eur. J. Biochem. 246:155-165(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon, Diaphragm, Embryo, and Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grammond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,


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Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 12 LDLEMLAXYIPMDDDFQL 30
Db 569 LDLEMLAXYIPMDDDFQL 587

RESULT 16
Q9X54 PRELIMINARY; PRT; 630 AA.
AC Q9X54;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 3 alpha (fragment).
GN Name=Hif3a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT "Cloning and Characterization of a Third Hypoxia Inducible Factor,
RT HIF3-alpha.";
RL J. Biol. Chem. 0:0-0(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99054547; PubMed=9840812;
RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT "Molecular characterization and chromosomal localization of a third
RT alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL Gene Expr. 7:205-213(1998).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF079153; AAF21782.1; JOINED.
DR EMBL; AF079140; AAF21782.1; JOINED.
DR EMBL; AF079141; AAF21782.1; JOINED.
DR EMBL; AF079143; AAF21782.1; JOINED.
DR EMBL; AF079145; AAF21782.1; JOINED.
DR EMBL; AF079147; AAF21782.1; JOINED.
DR EMBL; AF079149; AAF21782.1; JOINED.
DR EMBL; AF079151; AAF21782.1; JOINED.
DR EMBL; AF079152; AAF21782.1; JOINED.
DR EMBL; AF079150; AAF21782.1; JOINED.
DR EMBL; AF079148; AAF21782.1; JOINED.
DR EMBL; AF079146; AAF21782.1; JOINED.
DR EMBL; AF079144; AAF21782.1; JOINED.
DR EMBL; AF079142; AAF21782.1; JOINED.
DR HSP; Q99814; 1P97.
DR MGD; MGI:1859778; Hif3a.
DR GO; GO:0005634; C:nucleus; IC.
DR GO; GO:0003700; F:transcription factor activity; IPI.
DR GO; GO:001666; F:response to hypoxia; IDA.
DR GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAS.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
FT NON_TER 630
SQ SEQUENCE 630 AA; 69623 MW; 828EB2CBAE6D45B6 CRC64;

Query Match 52.9%; Score 81; DB 2; Length 630;
Best Local Similarity 88.9%; Pred. No. 0.015;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 13 LDLEMLAXYIPMDDDFQL 30
Db 569 LDLEMLAXYIPMDDDFQL 587

RESULT 17
Q8WX1 PRELIMINARY; PRT; 632 AA.
ID Q8WX1;
AC Q8WX1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibitory PAS domain protein.
GN Name=IPAS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng J.Q.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF463492; AAL69947.1; -.
DR HSP; Q16665; 1IQB.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 632 AA; 68963 MW; 9665B0AF3998F8EF CRC64;

Query Match 52.9%; Score 81; DB 2; Length 632;
Best Local Similarity 88.9%; Pred. No. 0.015;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 13 LDLEMLAXYIPMDDDFQL 30
Db 569 LDLEMLAXYIPMDDDFQL 502

RESULT 18
Q6STN6 PRELIMINARY; PRT; 643 AA.
ID Q6STN6;
AC Q6STN6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-4alpha.
GN Name=hif-4alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
```

DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 648 AA; 6995 MW; EBEC744BC3F148E CRC64;

Query Match 52.9%; Score 81; DB 2; Length 648;
Best Local Similarity 88.9%; Pred. No. 0.015;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 429 LDLEMLAPYSMDDDFQL 446

RESULT 20
Q9Z215 PRELIMINARY; PRT; 662 AA.
ID Q9Z215
AC Q9Z215
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypoxia inducible factor three alpha.
DE Name-Hif3a;
GN Name-Hif3a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99054547; PubMed=9840812;
RT Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RA "Molecular characterization and chromosomal localization of a third
RT alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL Gene Expr. 7:205-213(1998).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF060194; AAC72734.1; -.
DR HSSP; Q99814; 1P97.
DR MGD; MGI:1859778; Hif3a.
DR GO; GO:0005634; C:nucleus; IC.
DR GO; GO:0003700; P:transcription factor activity; IPI.
DR GO; GO:0003666; P:response to hypoxia; IDA.
DR GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 662 AA; 73012 MW; 58740A1B6993D3B5 CRC64;

Query Match 52.9%; Score 81; DB 2; Length 662;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 LDLEMLAXYIPMDDDFQL 30
|||||:|||||
Db 480 LDLEMLAPYSMDDDFQL 497

RESULT 21
Q9Y2N7 PRELIMINARY; PRT; 667 AA.
ID Q9Y2N7
AC Q9Y2N7
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative homolog of hypoxia inducible factor three alpha (Hypoxia-
DE inducible factor-3 alpha).
GN Name=HIF-3A;

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054582; AAHS4582.1; -;
DR HSSP; Q99814; IP97.
DR ZFIN; ZDB-GENE-040426-1315; hif1a1.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAC; 1.
DR PROSITE; PS00911; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
KW Hypothetical protein.
SQ SEQUENCE 571 AA; 63846 MW; 1BA8E4CC29F16672 CRC64;
Query Match 52.3%; Score 80; DB 2; Length 571;
Best Local Similarity 78.9%; Pred. No. 0.018;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 12 DLDLEMLAXYIPMDDDFQL 30
:||||:||||:||||:||||:
Db 430 ELDLMLAPYISMDDDFQL 448
RESULT 24
Q6EGR9 PRELIMINARY; PRT; 626 AA.
AC Q6EGR9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hif3a.
GN Name=hif3a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY330295; AAQ94179.1; -;
DR GO; GO:000634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY330295; AAQ94179.1; -;
DR GO; GO:000634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR

DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 626 AA; 70221 MW; EA12390DFECF90B9 CRC64;
Query Match 52.3%; Score 80; DB 2; Length 626;
Best Local Similarity 78.9%; Pred. No. 0.02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 12 DLDLEMLAXYIPMDDDFQL 30
:||||:||||:||||:||||:
Db 485 ELDLMLAPYISMDDDFQL 503
RESULT 25
Q9JHS2 PRELIMINARY; PRT; 662 AA.
AC Q9JHS2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypoxia inducible factor 3 alpha.
GN Name=Hif-3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA Kietmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
RT "Perivascular expression of the mRNA of the three hypoxia-inducible
RT factor a-subunits Hif-1a, Hif2a and Hif3a in rat liver.";
RL Biochem. J. 354:531-537(2001).
CC -|- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ277827; CAB96611.1; -;
DR HSSP; Q99814; IP97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 662 AA; 72887 MW; AC9672E340544010 CRC64;
Query Match 51.3%; Score 78.5; DB 2; Length 662;
Best Local Similarity 50.0%; Pred. No. 0.035;
Matches 18; Conservative 3; Mismatches 6; Indels 9; Gaps 1;
Qy 4 KKRQRERDL-----DLEMLAXYIPMDDDFQL 30
:||||:||||:||||:||||:
Db 462 RKNKMTETDLDAQDPDTPDLEMLAPYISMDDDFQL 497
RESULT 26
Q6GQ12 PRELIMINARY; PRT; 859 AA.
AC Q6GQ12;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DR

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DE MGC80468 protein.
GN Name=MGC80468;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Teshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skowood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Grimalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC072936; AAH72936.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR SEQUENCE 859 AA; 96956 MW; 59D477E1929A0AD6 CRC64;
Query Match 50.0%; Score 76.5; DB 2; Length 859;
Best Local Similarity 76.2%; Pred. No. 0.087;
Matches 16; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 11 RLDDLEMLAXYIPMD-DDFQL 30
:|||||:|||||:|||||
Db 516 KOLDLETLAPYIPMDGEDFQL 536

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RESULT 27
Q696W2 PRELIMINARY; PRT; 835 AA.
AC Q696W2;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Hypoxia-inducible factor 2 alpha.
GN Name=hif-2alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Kong R.Y.C., Wu R.S.S.;
RT "Molecular characterization of hypoxia-inducible factor-2alpha (hif-
RT 2alpha) gene in grass carp.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY577524; AAT76668.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR SEQUENCE 835 AA; 92830 MW; CAE59B9AFC785FD CRC64;
Query Match 48.7%; Score 74.5; DB 2; Length 835;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAXYIPMD-DDFQL 30
:|||||:|||||:|||||
Db 518 DLDLETLAPYIPMDGEDFQL 537
RESULT 28
Q6GL61 PRELIMINARY; PRT; 862 AA.
AC Q6GL61;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Epas1-prov protein.
GN Name=epas1-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

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RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC074648; AAH74648.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 862 AA; 97138 MW; C2976D62101531CE CRC64;
Query Match 48.7%; Score 74.5; DB 2; Length 862;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAXIYPMDDDFOL 30
DB 517 DLDLETLAPYIPMDGEDFOL 536
RESULT 29
QSGP97 PRELIMINARY; PRT; 862 AA.
AC Q6GP97;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MGC80589 protein.
GN Name=MGC80589;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC073244; AAH73244.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 862 AA; 97319 MW; 3AC8FB39032E9E60 CRC64;
Query Match 48.7%; Score 74.5; DB 2; Length 862;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 12 DLDLEMLAXIYPMDDDFOL 30
DB 518 DLDLETLAPYIPMDGEDFOL 537
RESULT 30
Q8QGM4 PRELIMINARY; PRT; 873 AA.
AC Q8QGM4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 2 alpha.
OS Fundulus heteroclitus (Killifish) (Mummichog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acantopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 NCBI_TaxID=8078;
 [1]_SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
 RA Powell W.H., Hahn M.E.;
 RT "Identification and functional characterization of Hypoxia-inducible
 factor 2alpha from the estuarine teleost, Fundulus heteroclitus;
 interaction of HIF2a with two ARNT2 splice variants.";
 RT J. Exp. Zool. 294:17-29(2002).
 RL -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC EMBL; AF402782; AAL95711.1; --
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; Nuc translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.
 DR PRINTS; PR00785; NCTRNSLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 873 AA; 96437 MW; BAC2CF0A0B4BC7B0 CRC64;
 Query Match 48.7%; Score 74.5; DB 2; Length 873;
 Best Local Similarity 80.0%; Pred. No. 0.17;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 12 LDLEMLAXIYIMD-DDFOL 30
 DB 541 LDLETLAPYIPMDGEDFOL 560
 RESULT 31
 ID Q96K34 PRELIMINARY; PRT; 632 AA.
 AC Q96K34;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14819.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Ovary;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakei K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AK027725; BAB55324.1; --
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; Nuc translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNSLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 632 AA; 68933 MW; A19F1ED3D05E7A71 CRC64;
 Query Match 48.4%; Score 74; DB 2; Length 632;
 Best Local Similarity 83.3%; Pred. No. 0.14;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 13 LDLEMLAXIYIPMDDDFOL 30
 DB 485 LDLEMLAPYISMGDDFOL 502
 RESULT 32
 ID Q6RYD1 PRELIMINARY; PRT; 163 AA.
 AC Q6RYD1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Endothelial PAS domain protein 1 (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=99823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ing N.H., Balog C.J., Wolfskill R.L.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AY485673; AAR37390.1; --
 FT NON_TER 1
 FT NON_TER 163
 SQ SEQUENCE 163 AA; 17207 MW; 679CD9F183CCAD3 CRC64;
 Query Match 46.1%; Score 70.5; DB 2; Length 163;

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Best Local Similarity 75.0%; Pred. No. 0.098; 1; Indels 1; Gaps 1;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXIYPMDD-DFQQL 30
:|||||:|||||:|||||
Db 118 ELDLETLAPYIPMDGEDFQL 137

RESULT 33
Q6RYDO PRELIMINARY; PRT; 164 AA.
AC Q6RYDO;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Endothelial PAS domain protein 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Ing N.H., Balog C.J., Wolfskill R.L.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485674; AAR37391.1; -.
FT NON_TER 1 164
FT NON_TER 164 164
SQ SEQUENCE 164 AA; 17405 MW; 49DBB95BA3D6D826 CRC64;

Query Match 46.1%; Score 70.5; DB 2; Length 164;
Best Local Similarity 75.0%; Pred. No. 0.099; 1; Indels 1; Gaps 1;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXIYPMDD-DFQQL 30
:|||||:|||||:|||||
Db 119 ELDLETLAPYIPMDGEDFQL 138

RESULT 34
Q9W7C6 PRELIMINARY; PRT; 867 AA.
AC Q9W7C6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DE Endothelial PAS domain protein 1.
GN Name=EPAS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed White Leghorn;
RX MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA Favier J., Kempf H., Corvol P., Gasc J.-M.;
RT "Cloning and expression pattern of EPAS1 in the chicken embryo.
RT Colocalization with tyrosine hydroxylase.";
RT FEBS Lett. 462:19-24(1999).
CC 1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF129813; RAD38358.1; -.
DR HSSP; Q99814; 1P97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 867 AA; 97133 MW; DE674A948DE11DCC CRC64;

Query Match 46.1%; Score 70.5; DB 2; Length 867;
Best Local Similarity 75.0%; Pred. No. 0.6;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXIYPMDD-DFQQL 30
:|||||:|||||:|||||
Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 35
PAS1_HUMAN STANDARD; PRT; 870 AA.
AC Q99814; Q86VA2; Q99630;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2)
DE (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)
DE (HIF-1 alpha-like factor) (HLF).
GN Name=EPAS1; Synonyms=HIF2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152468; PubMed=9000051;
RA Tian H., McKnight S.L., Russell D.W.;
RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT selectively expressed in endothelial cells.";
RL Genes Dev. 11:72-82(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSU=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdew G.H., Bradford C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway.";
RL J. Biol. Chem. 272:8581-8593(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSU=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
```

RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [4]
 RP TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
 RX MUTAGENESIS OF CVS-844.
 RA MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
 RA Ema W., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
 RA Poellinger L., Fujii-Kuriyama Y.;
 RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
 RT in response to hypoxia: their stabilization and redox signal-induced
 RT interaction with CBP/p300.";
 RL EMBO J. 18:1905-1914(1999).
 CC -!- FUNCTION: Transcription factor involved in the induction of oxygen
 CC regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
 CC the hypoxia response element (HRE) of target gene promoters.
 CC Regulates the vascular endothelial growth factor (VEGF) expression
 CC and seems to be implicated in the development of blood vessels and
 CC the tubular system of lung. May also play a role in the formation
 CC of the endothelium that gives rise to the blood brain barrier.
 CC Potent activator of the Tie-2 tyrosine kinase expression.
 CC Activation seems to require recruitment of transcriptional
 CC coactivators such as CREBBP and probably EP300. Interaction with
 CC redox regulatory protein APEX seems to activate CTAD.
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
 CC bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
 CC in placenta, lung and heart. Selectively expressed in endothelial
 CC cells.
 CC -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
 CC by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
 CC prolines promote interaction with VHL, initiating rapid
 CC ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
 CC preventing transcriptional activation (By similarity).
 CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 DR EMBL; U81984; AAB41495.1; -;
 DR EMBL; U51626; AAC51212.1; -;
 DR EMBL; BC051338; AAH51338.1; -;
 DR PDB; 1P97; NMR; A=237-350.
 DR TRANSFAC; T02718; -;
 DR Genew; HGNC:3374; EPAS1.
 DR MIM; 603349; -;
 DR GO; GO:0003705; F:RNA polymerase II transcription factor acti. . .; TAS.
 DR GO; GO:0003713; F:transcription coactivator activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006366; P:transcription from Pol II promoter; TAS.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001067; Nuc_translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 KW 3D-structure; Activator; Angiogenesis; Developmental protein;
 KW DNA-binding; Hydroxylator; Nuclear protein; Phosphorylation; Repeat;
 KW Transcription regulation.
 FT DNA BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 496 542 NTAD.
 FT DOMAIN 830 870 CTAD.
 FT DOMAIN 474 480 Poly-Ser.
 FT MOD_RES 405 405 Hydroxyproline (By similarity).
 FT MOD_RES 531 531 Hydroxyproline (By similarity).
 FT MOD_RES 840 840 Phosphoserine (By similarity).
 FT MOD_RES 847 847 3-hydroxyasparagine (By similarity).
 FT MUTAGEN 844 844 C->S: Abolishes hypoxia-inducible
 FT transcriptional activation of ctad.
 FT CONFLICT 60 60 A -> E (in Ref. 1).
 FT CONFLICT 539 539 D -> G (in Ref. 2).
 FT CONFLICT 601 601 H -> R (in Ref. 2).
 FT CONFLICT 693 693 D -> N (in Ref. 2).
 FT CONFLICT 716 716 E -> K (in Ref. 2).
 FT CONFLICT 722 722 L -> P (in Ref. 2).
 FT CONFLICT 765 765 F -> L (in Ref. 2).
 FT CONFLICT 769 769 P -> S (in Ref. 2).
 FT CONFLICT 844 844 C -> R (in Ref. 2).
 FT CONFLICT 847 847 N -> K (in Ref. 2).
 SQ SEQUENCE 870 AA; 96458 MW; 4838989598234FC1 CRC64;
 Query Match 46.1%; Score 70.5; DB 1; Length 870;
 Best Local Similarity 75.0%; Pred. No. 0.61;
 Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
 QY 12 DLDEMLAXYIPMD-DDFQL 30
 :||||:||||:||||:
 DB 523 ELDLETLAPYIPMDGDFQL 542
 RESULT 36
 Q9XTA4
 ID Q9XTA4 PRELIMINARY; PRT; 870 AA.
 AC Q9XTA4
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Endothelial PAS domain protein 1/hypoxia-inducible factor-2
 DE alpha.
 GN Name=EPAS1/HIF2 alpha;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Arterial;
 RX MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
 RA Hara S., Kobayashi C., Imura N.;
 RT "Molecular cloning of cDNA encoding hypoxia-inducible factor (HIF) -
 RT 1alpha and -2alpha of bovine arterial endothelial cells.";
 RL Biochim. Biophys. Acta 1445:237-243(1999).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AB018399; BAA78676.1; -;
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.

DR InterPro; IPR001067; Nuc_translocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR PRINTS; PR00785; NCTRNLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAS; 2.

SQ SEQUENCE 870 AA; 96168 MW; FEC602E6012D7712 CRC64;

Query Match 46.1%; Score 70.5; DB 2; Length 870;

Best Local Similarity 75.0%; Pred. No. 0.61;

Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXYIPMD-DDFQL 30

Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 37

Q9PTB3

ID Q9PTB3 PRELIMINARY; PRT; 870 AA.

AC Q9PTB3

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypoxia-inducible factor 2 alpha.

OS Coturnix coturnix (Common quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Coturnix.

OX NCBI_TaxID=9091;

RN NCBI_TaxID=9091;

RP SEQUENCE FROM N.A.

RX MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;

RA Elvert G., Ianz S., Kappel A., Flamme I.;

RT "mRNA cloning and expression studies of the quail homolog of HIF-2

alpha.";

RL Mech. Dev. 87:193-197(1999).

CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AF212989; AAF21052.1; -.

DR HSP; Q99814; 197.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR001092; HLH_basic.

DR InterPro; IPR001067; Nuc_translocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR00785; NCTRNLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAS; 2.

SQ SEQUENCE 870 AA; 97803 MW; 086AC8CF1639D77C CRC64;

Query Match 46.1%; Score 70.5; DB 2; Length 870;

Best Local Similarity 75.0%; Pred. No. 0.61;

Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXYIPMD-DDFQL 30

Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 38

PASI_MOUSE

ID PASI_MOUSE STANDARD; PRT; 874 AA.

AC P97481; O08787; O50046;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2

alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (HMLF)

DE (HIF-related factor) (HRF).

GN Name=Epas1; Synonyms=Hif2a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97152468; PubMed=9000051;

RA Tian H., McKnight S.L., Ruseell D.W.;

RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor

selectively expressed in endothelial cells.";

RL Genes Dev. 11:72-82(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Hypothalamus, and Skeletal muscle;

RX MEDLINE=97272213; PubMed=9113979; DOI=10.1073/pnas.94.9.4273;

RA Ena M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,

Fujii-Kuriyama Y.;

RT "A novel bHLH-PAS factor with close sequence similarity to hypoxia-

inducible factor 1alpha regulates the VEGF expression and is

potentially involved in lung and vascular development.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain capillary;

RX MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;

RA Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,

Risau W.;

RT "HRF, a putative basic helix-loop-helix-PAS-domain transcription

factor is closely related to hypoxia-inducible factor-1 alpha and

developmentally expressed in blood vessels.";

RL Mech. Dev. 63:51-60(1997).

RN [4]

RP SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.

RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;

RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,

Bruick R.K.;

RT "FTH-1 is an asparaginyl hydroxylase enzyme that regulates the

transcriptional activity of hypoxia-inducible factor.";

RL Genes Dev. 16:1466-1471(2002).

RN [5]

RP INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS

OF THR-844.

RX MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;

RA Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.;

RT "The transcriptional activation function of the HIF-like factor

requires phosphorylation at a conserved threonine.";

RL J. Biol. Chem. 277:23508-23514(2002).

RN [6]

RP HYDROXYLATION OF ASN-851.

RX MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;

RA Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.;

RT "Asparagine hydroxylation of the HIF transcription domain a hypoxic

switch.";

RL Science 295:858-861(2002).

CC -1- FUNCTION: Transcription factor involved in the induction of oxygen

regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within

the hypoxia response element (HRE) of target gene promoters.

CC Regulates the vascular endothelial growth factor (VEGF) expression

and seems to be implicated in the development of blood vessels and

the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier. Potent activator of the Tie-2 tyrosine kinase expression. Activation requires recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).

!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP.

!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels in lung, followed by heart, kidney, brain and liver. Predominantly expressed in endothelial cells. Also found in smooth muscle cells of the uterus, neurons, and brown adipose tissue. High expression in embryonic choroid plexus and kidney glomeruli.

!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost exclusively seen in endothelial cells of the intersegmental blood vessels separating the somites, the atrial and ventricular chambers of the heart, and the dorsal aorta. High expression also occurs in extra-embryonic membranes. In the developing brain of day 13 embryo, endothelial cells of the highly vascularized choroid plexus contain high levels of EPAS1.

!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).

!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation.

!- PTM: Phosphorylated on multiple sites in the CTAD.

!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; U81983; A841496.1; -
 EMBL; D89787; BAA20130.1; -
 EMBL; AF045160; AAC12871.1; -
 HSSP; Q16665; 1H2K.
 TRANSFAC; T02719; -
 MGD; MGI:109169; Epas1.
 InterPro; IPR001092; HLH basic.
 InterPro; IPR001067; Nuc_translocat.
 InterPro; IPR001610; PAC.
 InterPro; IPR000014; PAS.
 Pfam; PF00010; HLH; 1.
 Pfam; PF00785; PAS; 1.
 Pfam; PF00989; PAS; 1.
 PRINTS; PR00785; NCTRNLOCATR.
 SMART; SM00353; HLH; 1.
 SMART; SM00086; PAC; 1.
 SMART; SM00091; PAS; 2.
 TIGRFAMs; TIGR00229; sensory_box; 2.
 PROSITE; PS50888; HLH; FALSE_NEG.
 PROSITE; PS50112; PAS; 2.
 KW Activator; Angiogenesis; Developmental protein;
 KW Nuclear protein; Sequencing; DNA-binding; Hydroxylation;
 KW Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
 FT DNA_BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 NTAD.
 FT DOMAIN 834 874 CTAD.

FT DOMAIN 471 479 Poly-Ser.
 FT MOD_RES 405 Hydroxyproline (By similarity).
 FT MOD_RES 530 Hydroxyproline (By similarity).
 FT MOD_RES 844 Phosphothreonine.
 FT MOD_RES 851 3-hydroxyasparagine.
 FT MUTAGEN 530 P->A: Confers transcriptional activity at normoxia; when associated with A-851.
 FT MUTAGEN 844 T->A: Decreases interaction with CREBBP.
 FT MUTAGEN 851 N->A: Confers transcriptional activity at normoxia; when associated with A-530.
 FT CONFLICT 25 C->S (in Ref. 2).
 FT CONFLICT 191 K->KS (in Ref. 1).
 FT CONFLICT 439 VS->AA (in Ref. 3).
 FT CONFLICT 463 D->G (in Ref. 3).
 FT CONFLICT 654 G->V (in Ref. 2).
 FT CONFLICT 663 A->P (in Ref. 2).
 FT CONFLICT 669 S->W (in Ref. 1).
 FT CONFLICT 673 P->L (in Ref. 1).
 FT CONFLICT 678 P->L (in Ref. 1).
 FT CONFLICT 725 D->E (in Ref. 3).
 FT CONFLICT 731 P->L (in Ref. 3).
 FT CONFLICT 762 A->G (in Ref. 3).
 FT CONFLICT 786 P->L (in Ref. 3).
 FT CONFLICT 791 S->F (in Ref. 3).
 FT CONFLICT 794 S->N (in Ref. 3).
 SQ SEQUENCE 874 AA; 96712 MW; A6PFA490AE43640C CRC64;
 Query Match 46.1%; Score 70.5; DB 1; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.61; Mismatches 3; Indels 1; Gaps 1;
 Matches 15; Conservative 3;
 QY 12 DLDLEMLAXYIPMD-DDFQL 30
 :|||||:|||||:|||||
 Db 522 ELDTLTLAPYIPMDGEDFQL 541

RESULT 39
 ID_PASI_RAT STANDARD; PRT; 874 AA.
 AC Q9JHS1;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha).
 GN Name=Epas1; Synonyms=Hif2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RT Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivascular expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 CC **!- FUNCTION:** Transcription factor involved in the induction of oxygen regulated genes. Binds to core DNA sequence 5'-(AG)CGTG-3' within the hypoxia response element (HRE) of target gene promoters. Regulates the vascular endothelial growth factor (VEGF) expression and seems to be implicated in the development of blood vessels and the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier.
 CC Potent activator of the Tie-2 tyrosine kinase expression.
 CC Activation seems to require recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 CC **!- SUBUNIT:** Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT (By similarity).
 CC **!- SUBCELLULAR LOCATION:** Nuclear (Potential).

-1- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).

-1- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation (By similarity).

-1- PTM: Phosphorylated on multiple sites in the CTAD (By similarity). -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain. -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains. -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; AJ277828; CAB96612.1; -
 HSSP; Q16665; 1H2K.
 InterPro; IPR001092; HLH basic.
 InterPro; IPR001067; Nuc_translocat.
 InterPro; IPR001610; PAC.
 InterPro; IPR000014; PAS.
 Pfam; PF00010; HLH; 1.
 Pfam; PF00785; PAS; 1.
 Pfam; PF00989; PAS; 2.
 PRINTS; PR00785; NCTRNLOCATR.
 SMART; SM00353; HLH; 1.
 SMART; SM00086; PAC; 1.
 SMART; SM00091; PAS; 2.
 TIGRFAMs; TIGR00229; sensory_box; 2.
 PROSITE; PS50888; HLH; FALSE_NEG.
 PROSITE; PS0112; PAS; 2.
 Activator; Angiogenesis; Developmental protein; DNA-binding;
 Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
 Transcription regulation.
 DNA BIND 15 27 Basic motif.
 DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 CTAD.
 FT DOMAIN 834 874 Poly-Ser.
 FT DOMAIN 474 479 Hydroxyproline (By similarity).
 FT MOD_RES 405 405 Hydroxyproline (By similarity).
 FT MOD_RES 530 530 Hydroxyproline (By similarity).
 FT MOD_RES 844 844 Phosphothreonine (By similarity).
 FT MOD_RES 851 851 3-hydroxyasparagine (By similarity).
 SQ SEQUENCE 874 AA; 96718 MW; A1FF08EB24369796 CRC64;

Query Match 46.1%; Score 70.5; DB 1; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.61;
 Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXYIPMD-DDFQL 30
 :|||||:|||||:|||||
 Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 40
 Q6PEU2 PRELIMINARY; PRT; 874 AA.
 AC Q6PEU2
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Endothelial PAS domain protein 1.
 GN Name=Epas1;

Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson W.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC057870; AAH57870.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001067; Nuc_translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00785; PAS; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 874 AA; 96636 MW; 2E6D7603A678EACE CRC64;

Query Match 46.1%; Score 70.5; DB 2; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.61;
 Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 12 DLDLEMLAXYIPMD-DDFQL 30
 :|||||:|||||:|||||
 Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 41
 Q71939 PRELIMINARY; PRT; 71 AA.
 AC Q71939
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tat protein (fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Michael N.L.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 CC trans-activating responsive sequence (TAR) RNA element and
 CC activates transcription initiation and/or elongation from the LTR
 CC promoter (By similarity).
 DR EMBL; U24453; AAA79589.1; -;
 DR HSSP; P12506; ITBC.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PR00055; HIVTATDOMAIN.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 KW Transcription regulation.
 FT NON TER 71
 SQ SEQUENCE 71 AA; 8307 MW; A3EFC2840AFF2A50 CRC64;
 Query Match 42.2%; Score 64.5; DB 2; Length 71;
 Best Local Similarity 58.3%; Pred. No. 0.27;
 Matches 14; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 OY 1 YGRKKRRQRRR-DLDLEMLAXIYP 23
 DB 47 YGRKKRRQRRRAPQDSQTYQAYLP 70
 RESULT 42
 Q71945 PRELIMINARY; PRT; 71 AA.
 AC Q71945;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Michael N.L.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 CC trans-activating responsive sequence (TAR) RNA element and
 CC activates transcription initiation and/or elongation from the LTR
 CC promoter (By similarity).
 DR EMBL; U24454; AAA79595.1; -;
 DR HSSP; P12506; ITBC.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 KW Transcription regulation.
 FT NON TER 71
 SQ SEQUENCE 71 AA; 8307 MW; A3EFC2840AFF2A50 CRC64;
 Query Match 42.2%; Score 64.5; DB 2; Length 71;
 Best Local Similarity 58.3%; Pred. No. 0.27;
 Matches 14; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

OY 1 YGRKKRRQRRR-DLDLEMLAXIYP 23
 DB 47 YGRKKRRQRRRAPQDSQTYQAYLP 70
 RESULT 43
 Q69628 PRELIMINARY; PRT; 72 AA.
 AC Q69628;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95264414; PubMed=7745674;
 RA Diaz R.S.; Sabino E.C.; Mayer A.; Mosley J.W.; Busch M.P.;
 FT "Dual human immunodeficiency virus type 1 infection and recombination
 FT in a dually exposed transfusion recipient. The Transfusion Safety
 FT Study Group.";
 RL J. Virol. 69:3273-3281(1995).
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 CC trans-activating responsive sequence (TAR) RNA element and
 CC activates transcription initiation and/or elongation from the LTR
 CC promoter (By similarity).
 DR EMBL; U11191; AAA78877.1; -;
 DR HSSP; P04610; 1JFW.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PR00055; HIVTATDOMAIN.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 KW Transcription regulation.
 FT NON TER 72
 SQ SEQUENCE 72 AA; 8428 MW; 4A00C4BF93D0E86 CRC64;
 Query Match 41.5%; Score 63.5; DB 2; Length 72;
 Best Local Similarity 65.2%; Pred. No. 0.38;
 Matches 15; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 OY 1 YGRKKRRQRRRDL-DLEMLAXIYI 22
 DB 47 YGRKKRRQRRRALKDSETHQAYL 69
 RESULT 44
 Q71264 PRELIMINARY; PRT; 101 AA.
 AC Q71264;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Tat protein.
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oelrichs R.B.; McPhee D.A.; Deacon N.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
 CC trans-activating responsive sequence (TAR) RNA element and
 CC activates transcription initiation and/or elongation from the LTR


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CC promoter (By similarity).
DR EMBL; AF042102; JAFD.
DR HSSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006355; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
Transcription regulation.
SQ SEQUENCE 101 AA; 11618 MW; AE0717D0D3C01E1 CRC64;

Query Match 40.8%; Score 62.5; DB 2; Length 101;
Best Local Similarity 58.3%; Pred. No. 0.76;
Matches 14; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Oy 1 YGRKKRQRRR-DLDEMLAXYIP 23
Dy 47 YGRKKRQRRR-PQDSQTHIYLP 70

RESULT 45
Q8ADC2 PRELIMINARY; PRT; 86 AA.
AC Q8ADC2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tat protein.
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22375625; PubMed=12487816; DOI=10.1089/08992202320886325;
RA Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA Kigozi G., Kiwanuka N., Phillips J.B., Meehan M., Lutalo T.,
RA Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA McCutchan F.E.;
RT "Among 46 near full length HIV type 1 genome sequences from Rakai
RT District, Uganda, subtype D and AD recombinants predominate.";
RL AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Harris M.E., Birx D.L., Robb M.L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Lutalo T.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Meehan M., Wawer M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
trans-activating responsive sequence (TAR) RNA element and
activates transcription initiation and/or elongation from the LTR
promoter (By similarity).
DR EMBL; AF484516; AAN73784.1; -.
DR HSSP; P04613; 1KSK.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
KW Activator; Nuclear protein; RNA-binding; Transcription;
Transcription regulation.
SQ SEQUENCE 86 AA; 9905 MW; 01C995B36AE0161A CRC64;

Query Match 40.5%; Score 62; DB 2; Length 86;
Best Local Similarity 53.8%; Pred. No. 0.75;
Matches 14; Conservative 0; Mismatches 2; Indels 10; Gaps 1;

Oy 1 YGRKKRQRRR-DLDEMLAXYIPMD 26
Dy 47 YGRKKRQRRS-----PQDD 62

RESULT 46
P88699 PRELIMINARY; PRT; 72 AA.
AC P88699;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Quinones-Mateu M.E., Domingo E.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
trans-activating responsive sequence (TAR) RNA element and
activates transcription initiation and/or elongation from the LTR
promoter (By similarity).
DR EMBL; U80465; AAB39115.1; -.
DR HSSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8342 MW; ED2C18A34DA4B591 CRC64;

Query Match 39.9%; Score 61; DB 2; Length 72;
Best Local Similarity 91.7%; Pred. No. 0.85;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRKKRQRRRD 12
Dy 47 YGRKKRQRRRD 58

RESULT 47
Q6EK47 PRELIMINARY; PRT; 101 AA.
AC Q6EK47;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tat protein.
GN Name=tat;
OS Human immunodeficiency virus 1.

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RN [2]
RP SEQUENCE FROM N.A.
RA Harris M.E., Birt D.L., Robb M.L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Lutalo T.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Meshen M., Waver M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter (By similarity).
CC EMBL; AF484504; AAN73676.1; -.
DR HSSP; P04613; 1K5K.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 86 AA; 9858 MW; 29052AD5D90A8498 CRC64;

Query Match      38.6%; Score 59; DB 2; Length 86;
Best Local Similarity 53.8%; Pred. No. 2;
Matches 14; Conservative 0; Mismatches 2; Indels 10; Gaps 1;

Qy 1 YGRKKRQRRLDLEMLAXYIPMDD 26
Db 47 YGRKKRQRRLDLEMLAXYIPMDD 62

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Search completed: February 8, 2005, 20:09:56
 Job time : 150.947 secs